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(54) **DNA ENCODING IL-2 FUSION PROTEINS WITH MODULATED SELECTIVITY**  
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(57) **ABSTRACT**

The invention provides cytokine fusion proteins with an increased therapeutic index, and methods to increase the therapeutic index of such fusion proteins. The fusion proteins of the invention are able to bind to more than one type of cytokine receptor expressed on cells and also bind to more than one cell type. In addition, the fusion proteins of the invention exhibit a longer circulating half-life in a patient's body than the corresponding naturally occurring cytokine.



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Figure 1A

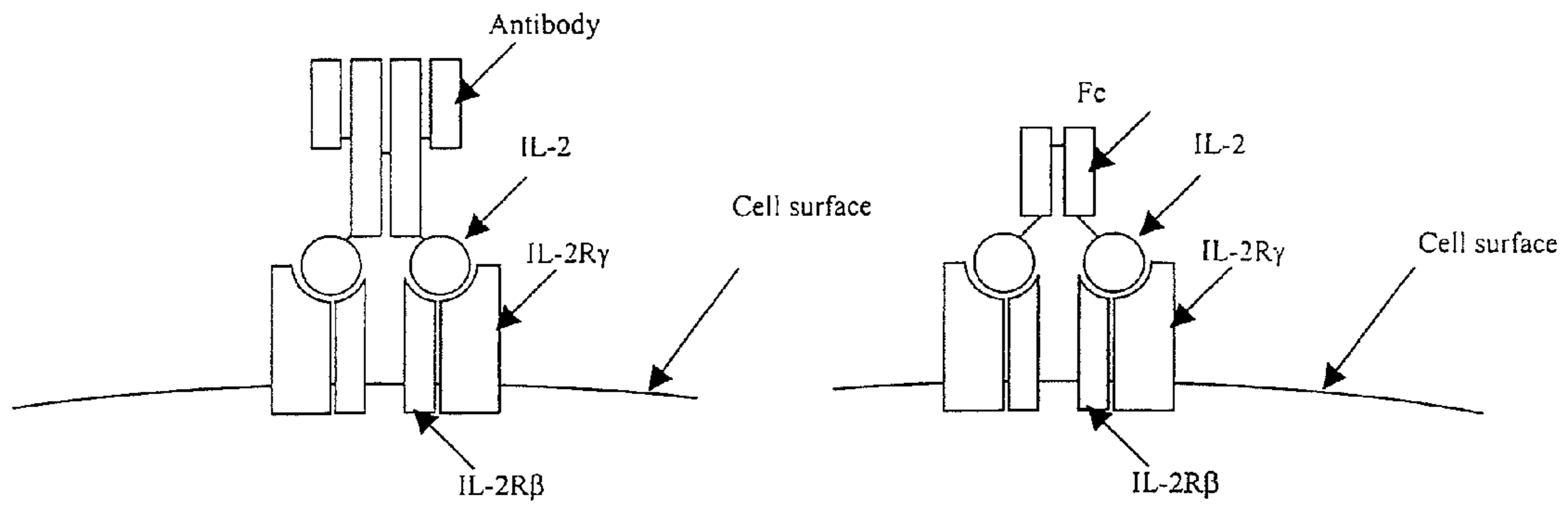


Figure 1B

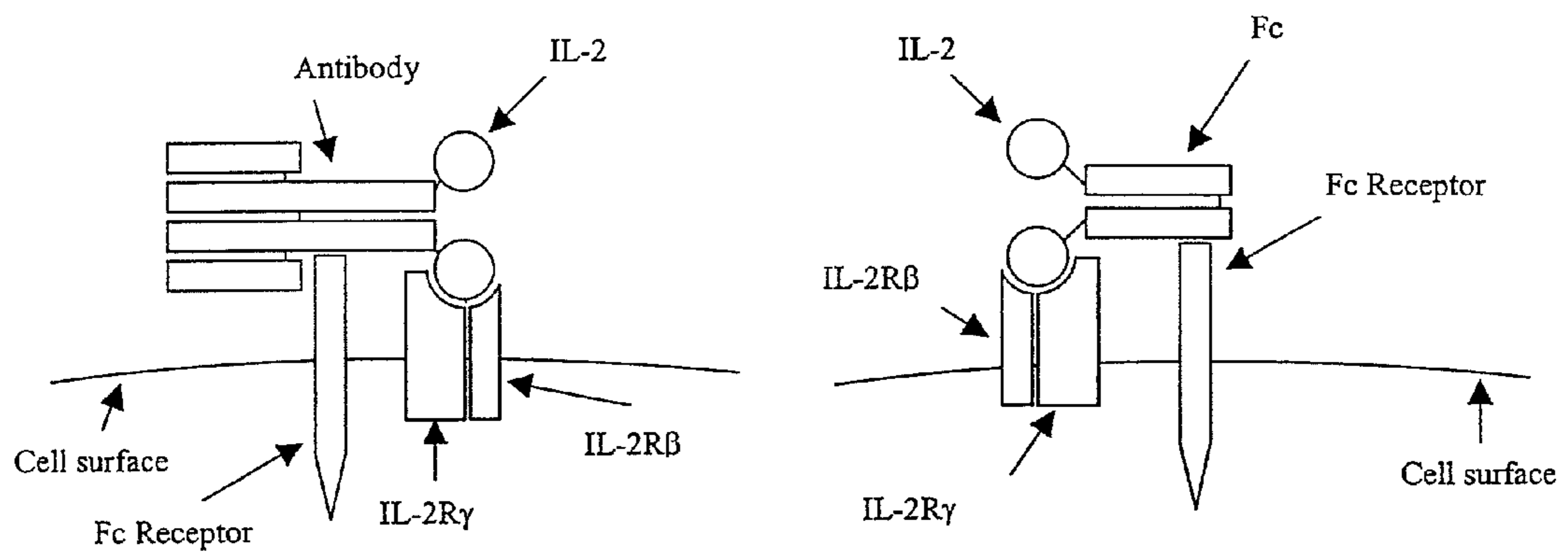
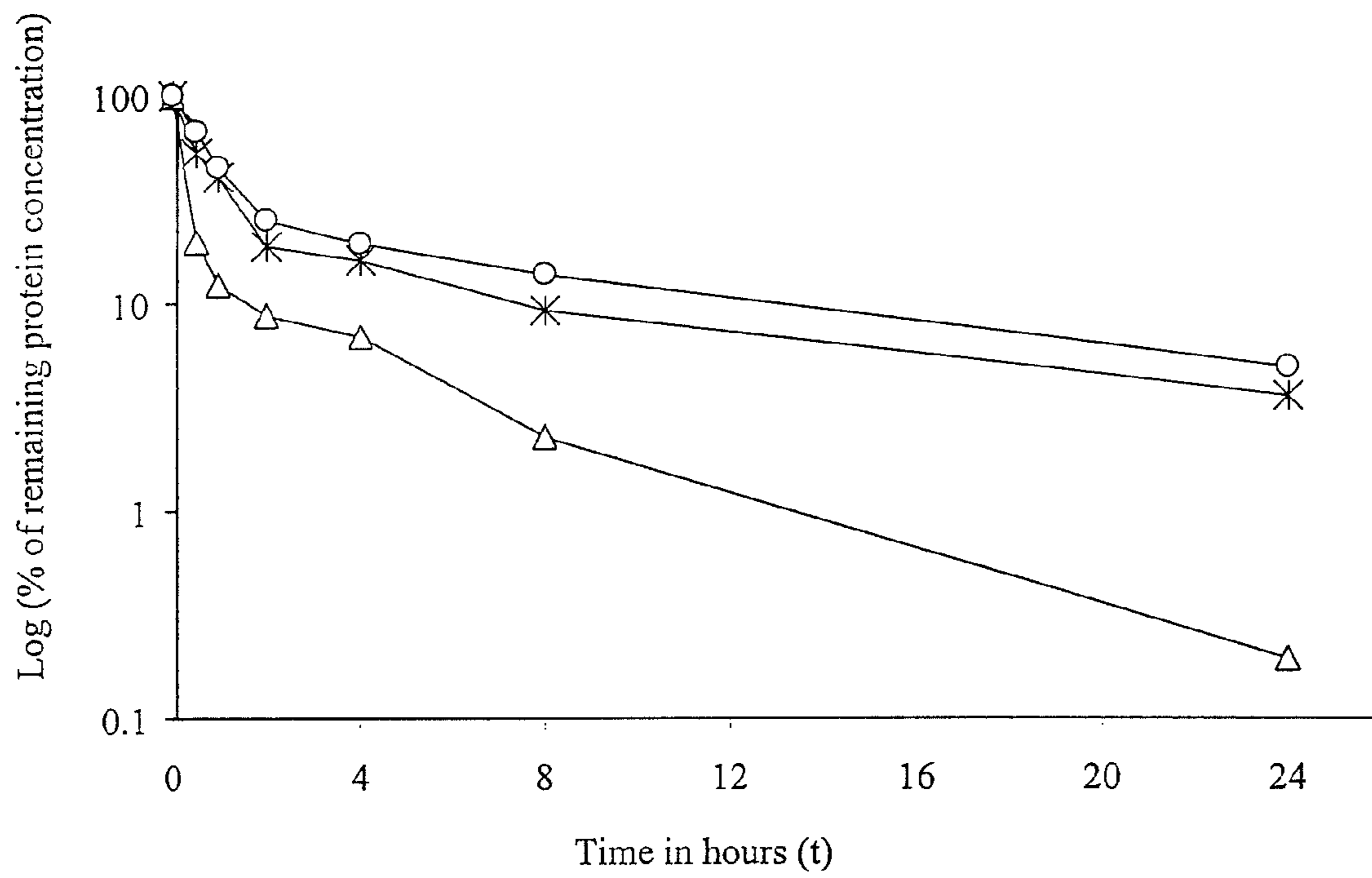




Figure 2





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## DNA ENCODING IL-2 FUSION PROTEINS WITH MODULATED SELECTIVITY

### REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. Ser. No. 11/581,663, filed Oct. 16, 2006, which is a continuation of U.S. Ser. No. 10/310,719, filed Dec. 4, 2002, now U.S. Pat. No. 7,186,804, which claims priority to, and the benefit of U.S. Ser. No. 60/337,113, filed Dec. 4, 2001, and U.S. Ser. No. 60/371,966, filed Apr. 12, 2002, the entire disclosures of each of which are incorporated by reference herein.

### FIELD OF THE INVENTION

The present invention relates generally to fusion proteins containing a cytokine, and methods to increase the therapeutic effectiveness of such fusion proteins. More specifically, the present invention relates to cytokine fusion proteins that exhibit a longer circulating half-life in a patient's body than the corresponding naturally occurring cytokine and that have improved therapeutic properties. In particular, the invention relates to IL2 fusion protein with improved therapeutic characteristics.

### BACKGROUND

Interleukin-2 (IL-2) is a potent cytokine that acts on the immune system to generate primarily a cell-mediated immune response. Under the appropriate conditions, IL-2 is produced locally at high concentrations near the site of an antigen in order to supply the necessary co-stimulatory signals for generating an immune response to the antigen. Because of its role in the growth and differentiation of T cells, IL-2 has been a candidate in immunotherapeutic approaches to treating tumors. In addition to stimulating T cells, IL-2 has also been shown to stimulate B cells, NK cells, lymphokine activated killer cells (LAK), monocytes, macrophages and dendritic cells.

IL-2 is an approved therapeutic agent for the treatment of metastatic renal carcinoma and metastatic melanoma but its use is restricted due to severe toxic side effects, which include fever, nausea, vascular leakage and hypotension. Among the various toxic effects observed with IL-2 administration, the one toxic effect that is the least desirable and is believed to substantially interfere with IL-2 therapy is vascular leak syndrome (VLS) and the complications associated with it.

Therefore, there remains a need in the art to further enhance the therapeutic usefulness of IL-2 proteins.

### SUMMARY OF THE INVENTION

The present invention is based, in part, upon the identification of mutations in the IL-2 moiety of an IL-2 fusion protein to increase the maximum tolerated dose of the protein relative to the dose of maximal effectiveness for that protein when administered to a patient. Preferred fusion proteins are able to bind by distinct interactions to more than one receptor species expressed on the same cell in the patient's body. Preferred cytokine fusion proteins include a cytokine that is able to bind to more than one type of cytokine receptor complex and to more than one cell type. The invention also provides methods to identify particular cytokine fusion protein variants with useful properties.

The present invention provides fusion proteins comprising a non-IL-2 moiety fused to a mutant IL-2 moiety, where the fusion protein exhibits a greater selectivity than a reference

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protein including the non-IL-2 moiety fused to a non-mutant IL-2 moiety, and where the selectivity is measured as a ratio of activation of cells expressing IL-2R $\alpha\beta\gamma$  receptor relative to activation of cells expressing IL-2R $\beta\gamma$  receptor.

5 The mutant IL-2 moiety of the fusion proteins includes a mutation in one or more amino acids of the mature human IL-2 protein. In one embodiment, fusion proteins according to the invention include an amino acid substitution at one or more amino acid positions in the IL-2 moiety. In another embodiment, fusion proteins of the invention include deletions of amino acids at one or more amino acid positions in the IL-2 moiety. In yet another embodiment, fusion proteins of the invention include modifications of one or more amino acids in the IL-2 moiety of the fusion proteins.

15 Mutations in the fusion proteins of the invention alter the selectivity of fusion proteins relative to a reference fusion protein, where the selectivity is measured as a ratio of activation of cells expressing IL-2R $\alpha\beta\gamma$  receptor relative to activation of cells expressing IL-2R $\beta\gamma$  receptor. Mutations in the fusion proteins can also result in a differential effect on the fusion protein's affinity for IL-2R $\beta\gamma$  receptor relative to the fusion protein's affinity for IL-2R $\alpha\beta\gamma$  receptor. Preferred mutations or alterations reduce a fusion protein's activation of cells expressing IL-2R $\beta\gamma$  receptor relative to the fusion protein's activation of cells expressing IL-2R $\alpha\beta\gamma$  receptor.

25 Preferred fusion proteins of the invention generally exhibit a differential effect that is greater than about 2-fold. In one aspect, the differential effect is measured by the proliferative response of cells or cell lines that depend on IL-2 for growth. This response to the fusion protein is expressed as an ED50 value, which is obtained from plotting a dose response curve and determining the protein concentration that results in a half-maximal response. The ratio of the ED50 values obtained for cells expressing IL-2R $\beta\gamma$  receptor to cells expressing IL-2R $\alpha\beta\gamma$  receptor for a fusion protein of the invention relative to the ratio of ED50 values for a reference fusion protein gives a measure of the differential effect for the fusion protein.

30 The selectivity of fusion proteins of the invention may be measured against a reference fusion protein comprising the same non-IL-2 moiety as in the fusion protein fused to a non-mutant IL-2 moiety. In a preferred embodiment, a differential effect measured for the fusion proteins of the invention, as described above, is between about 5-fold and about 10-fold. Preferably, the differential effect exhibited by the fusion proteins of the invention is between about 10-fold and about 1000-fold.

35 In an alternative preferred embodiment, the selectivity of the fusion protein is compared to the selectivity of a reference fusion protein that comprises the same non-IL-2 moiety as in the fusion protein fused to an IL-2 moiety including mature human IL-2 with an amino acid substitution at position 88 changing an asparagine to an arginine (N88R). Fusion proteins of the invention that have an improved therapeutic index include fusion proteins having a selectivity close to that of N88R but between about 0.1% to about 100% of the selectivity of a reference fusion protein with the N88R amino acid substitution. In another embodiment, fusion proteins of the invention have a selectivity between about 0.1% to about 30% of the selectivity of a reference fusion protein with the N88R amino acid substitution in the IL-2 moiety. Fusion proteins of the invention also include fusion proteins that have a selectivity between about 1% to about 20% of the selectivity of the reference fusion protein with the N88R amino acid substitution in the IL-2 moiety. Selectivity of fusion proteins of the invention can also be between about 2% to about 10% of the



selectivity of the reference fusion protein including the N88R amino acid substitution in the mature human IL-2 moiety.

Fusion proteins of the invention have a serum half-life that is longer than the serum half life of mature human IL-2 protein. The long serum half-life of fusion proteins of the invention can be attributed to the non-IL-2 moiety of the fusion protein. For example, in one embodiment, the non-IL-2 moiety of a fusion protein of the invention is albumin. In another embodiment, the non-IL2 moiety of a fusion protein of the invention is an antibody domain including, for example, variants of the KS-1/4 antibody domain, variants of the NHS76 antibody domain and variants of the 14.18 antibody domain. The antibody domain can also be selected from a variety of other antibodies, for example, antibodies against various tumor and viral antigens.

In a preferred embodiment, a differential effect measured for the fusion proteins of the invention, as described above, is between about 5-fold and about 10-fold. Preferably, the differential effect exhibited by the fusion proteins of the invention is between about 10-fold and about 1000-fold.

It is useful to mutate amino acids in the IL-2 moiety of fusion proteins of the invention that result in a differential effect which is 2-fold or greater. Different amino acid mutations in the IL-2 moiety result in a differential effect greater than about 2-fold, between about 5-fold and about 10-fold, or preferably between about 10-fold and about 1000-fold. In a preferred embodiment, the amino acid mutation is a substitution of the aspartic acid corresponding to position 20 of the mature human IL-2 moiety with a threonine (D20T). In yet another preferred embodiment, the amino acid mutation is a substitution of the asparagine at position 88 of the mature human IL-2 protein with an arginine (N88R). Fusion proteins of the invention can also include mutations at more than one amino acid positions. In one embodiment, a fusion protein according to the invention includes amino acid substitutions changing an asparagine to an arginine at position 88, a leucine to a threonine at position 85 and an isoleucine to a threonine at position 86 of the mature human IL-2 protein.

Mutations of amino acids at certain positions in the IL-2 moiety results in a differential effect that is greater than about 2-fold. It is useful to mutate amino acids corresponding to positions K8, Q13, E15, H16, L19, D20, Q22, M23, N26, H79, L80, R81, D84, N88, I92, and E95 of the mature human IL-2 protein. Additional useful amino acid positions that can be mutated are L25, N31, L40, M46, K48, K49, D109, E110, A112, T113, V115, E116, N119, R120, I122, T123, Q126, S127, S130, and T131 of the mature human IL-2 protein. Preferred amino acid positions that are mutated in fusion proteins of the invention include D20, N88, and Q126.

In one embodiment, one or more amino acid at the preferred positions listed above are mutated in the fusion proteins. In a preferred embodiment, the amino acid asparagine at position 88 is substituted with an arginine (N88R). In another preferred embodiment, the amino acid aspartic acid at position 20 is substituted with a threonine (D20T). In yet another preferred embodiment, the glutamine at position 126 is substituted with an aspartic acid (Q126D). The various amino acid substitutions result in a selectivity in the activity of fusion proteins of the invention for IL-2R $\alpha\beta\gamma$  receptor bearing cells relative to IL-2R $\beta\gamma$  receptor bearing cells, which can be reflected in the fusion protein's affinity for an IL-2R $\beta\gamma$  receptor relative to the fusion protein's affinity for an IL-2R $\alpha\beta\gamma$  receptor.

Fusion proteins with mutations at one or more amino acid positions described above have a differential effect that is greater than about 2-fold. Preferably, the differential effect is

between about 5-fold and about 10-fold and more preferably between about 10-fold and about 1000-fold.

In addition to mutating amino acids in the IL-2 moiety, amino acids in the non-IL-2 moiety can also be mutated. In a preferred embodiment, the non-IL-2 moiety is an antibody domain. The antibody domain can be selected from a variety of different immunoglobulin (Ig) antibodies, preferably IgG antibodies, including for example, IgG gamma 1, IgG gamma 2 and IgG gamma 4 antibody domains, or any combination of these antibody domains. As used herein, the terms "antibody" and "immunoglobulin" are understood to mean (i) an intact antibody (for example, a monoclonal antibody or polyclonal antibody), (ii) antigen binding portions thereof, including, for example, an Fab fragment, an Fab' fragment, an (Fab')<sub>2</sub> fragment, an Fv fragment, a single chain antibody binding site, an sFv, (iii) bi-specific antibodies and antigen binding portions thereof, and (iv) multi-specific antibodies and antigen binding portions thereof. In proteins of the invention, an immunoglobulin Fc region can include at least one immunoglobulin constant heavy region, for example, an immunoglobulin constant heavy 2 (CH2) domain, an immunoglobulin constant heavy 3 (CH3) domain, and depending on the type of immunoglobulin used to generate the Fc region, optionally an immunoglobulin constant heavy 4 (CH4) domain, or a combination of the above. In particular embodiments, the immunoglobulin Fc region may lack an immunoglobulin constant heavy 1 (CH1) domain. Although the immunoglobulin Fc regions may be based on any immunoglobulin class, for example, IgA, IgD, IgE, IgG, and IgM, immunoglobulin Fc regions based on IgG are preferred. An antibody moiety included in a fusion protein of the invention is preferably human, but may be derived from a murine antibody, or any other mammalian or non-mammalian immunoglobulin. It is contemplated that an Fc region used in a fusion protein of the invention may be adapted to the specific application of the molecule. In one embodiment, the Fc region is derived from an immunoglobulin  $\gamma$ 1 isotype or a variant thereof. In another embodiment, the Fc region is derived from an immunoglobulin  $\gamma$ 2 isotype or a variant thereof. In further embodiments, the Fc region may be derived from an immunoglobulin  $\gamma$ 3 isotype or a variant thereof. The Fc region may comprise a hinge region that is derived from a different immunoglobulin isotype than the Fc region itself. For example, the Fc region may be derived from an immunoglobulin  $\gamma$ 2 isotype and include a hinge region derived from an immunoglobulin  $\gamma$ 1 isotype or a variant thereof. In yet another preferred embodiment of the invention, the Fc region is derived from an immunoglobulin  $\gamma$ 4 isotype. Immunoglobulin  $\gamma$ 4 isotypes that have been modified to contain a hinge region derived from an immunoglobulin  $\gamma$ 1 isotype or a variant thereof are particularly preferred.

In one embodiment, fusion proteins of the invention comprise mutations in the Ig moiety. A useful mutation is a mutation in the IgG gamma 1 sequence QYNSTYR (SEQ ID NO: 1), changing the N to a Q; a particularly useful mutation is a mutation in the gamma 2 or 4 sequence QFNST (SEQ ID NO: 2), changing the dipeptide motif FN to AQ.

The invention also features DNA constructs encoding various fusion proteins of the invention. The fusion proteins of the invention are particularly useful for treating cancer, viral infections and immune disorders.



These and other objects, along with advantages and features of the invention disclosed herein, will be made more apparent from the description, drawings, and claims that follow.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 illustrates the fusion of a cytokine to a second protein moiety that alters the natural binding characteristics of the cytokine. FIG. 1A depicts the fusion partner to IL-2 as a dimeric molecule, such as an antibody or the Fc portion of an Fc-containing fusion protein, and therefore two molecules of IL-2 are brought to the cell surface when the IL-2 moiety of the fusion protein interacts with its receptor. FIG. 1B illustrates a second mechanism that produces the same effect.

FIG. 2 shows typical pharmacokinetic profiles of the fusion protein immunocytokine huKS-IL2 (represented by triangles) and two variants, huKS-ala-IL2 (represented by circles) and huKS-ala-IL2(N88R) (represented by stars).

#### DETAILED DESCRIPTION OF THE INVENTION

The invention provides methods and compositions that enhance the therapeutic index of IL-2 fusion proteins and IL-2 immunocytokines in particular. According to the invention, the therapeutic index of a therapeutic molecule is a measure of the ratio of the maximum tolerated dose of a molecule divided by the dose of maximal effectiveness for that molecule. The invention includes improved variants of IL-2 immunocytokines that exhibit a significantly longer circulating half-life compared to free IL-2. The invention also provides IL-2 fusion proteins, and in particular IL-2 immunocytokines, that exhibit a selective IL-2 response, reflected by reduced activation of cells with various effector functions by the fusion proteins of the invention, which is a leading cause of the toxic effects of IL-2. In addition, the invention provides IL-2 fusion proteins with improved activity. An IL-2 fusion protein of the invention includes changes at one or more amino acid positions that alter the relative affinity of the IL-2 fusion protein for different IL-2 receptors, resulting in altered biological properties of the IL-2 fusion protein. The invention is useful to reduce or minimize any toxicity associated with IL-2 therapy. Regardless of the underlying mechanism of any given IL-2 toxicity, such as VLS, the toxicity results in part from the fact that IL-2 is administered intravenously and therefore acts systemically within the body, even though the effect of IL-2 is desired at a specific site. This problem is exacerbated by the fact that a systemic administration of IL-2 requires a much higher dose than a localized administration would, which in turn may promote toxicities that would not be seen at lower doses. The invention provides IL-2 fusion proteins with reduced toxicity. The invention also provides methods for making IL-2 fusion proteins with reduced toxicity.

In general, the invention is useful for fusion proteins including an IL-2 moiety fused to a non-IL-2 moiety. According to the invention, a non-IL-2 moiety can be a synthetic or a natural protein or a portion or variant (including species, allelic and mutant variants) thereof. Preferred non-IL-2 moieties include Fc and albumin moieties. According to the invention, an IL-2 moiety can be a natural IL-2 molecule or a portion or variant (including species, allelic and mutant variants) thereof that retains at least one IL-2 activity or function (an IL-2 moiety can be an IL-2 that is modified to have a different IL-2 receptor binding affinity according to the invention).

According to the invention, cells respond to IL-2 through specific cell surface receptors (IL-2R), which exist in two forms. The high affinity receptor is heterotrimeric, consisting of  $\alpha$ ,  $\beta$  and  $\gamma$  subunits; the intermediate affinity receptor is heterodimeric, consisting of  $\beta$  and  $\gamma$  subunits. Binding constants of IL-2 for these two forms of IL-2R differ by two orders of magnitude. Signal transduction is mediated on the cytoplasmic side of the receptor through interactions within the  $\beta\gamma$  complex. Different cell types express the  $\alpha$ ,  $\beta$  and  $\gamma$  subunits in varying amounts. For instance, activated T cells express all of the subunits to form the high affinity IL-2R $\alpha\beta\gamma$ , whereas mature resting T cells and NK cells express the  $\beta$  and  $\gamma$  subunits to give the intermediate affinity IL-2R $\beta\gamma$ . Thus, cells require different levels of exposure to IL-2 for stimulation, and conversely, by regulating IL-2 activity within a specific cellular context, the nature of an immune response can be controlled.

Methods and compositions of the invention are particularly useful in the context of IL-2 fusion proteins such as IL-2 bearing immunocytokines. According to the invention, IL-2 bearing immunocytokines are synthetic molecules that have been shown to significantly increase the efficacy of IL-2 therapy by directly targeting IL-2 into a tumor microenvironment. Immunocytokines are fusion proteins consisting of an antibody moiety and a cytokine moiety, such as an IL-2 moiety. According to the invention, an antibody moiety can be a whole antibody or immunoglobulin or a portion, or variant (including species, allelic and mutant variants) thereof that has a biological function such as antigen specific binding affinity. Similarly, a cytokine moiety of the invention can be a natural cytokine or a portion or variant (including species, allelic and mutant variants) thereof that retains at least some cytokine activity. The benefits of an immunocytokine therapy are readily apparent. For example, an antibody moiety of an immunocytokine recognizes a tumor-specific epitope and results in targeting the immunocytokine molecule to the tumor site. Therefore, high concentrations of IL-2 can be delivered into the tumor microenvironment, thereby resulting in activation and proliferation of a variety of immune effector cells mentioned above, using a much lower dose of the immunocytokine than would be required for free IL-2. In addition, the increased circulating half-life of an immunocytokine compared to free IL-2 contributes to the efficacy of the immunocytokine. And finally, the natural effector functions of an antibody also may be exploited, for instance by activating antibody dependent cellular cytotoxicity (ADCC) in Fc $\gamma$ RIII bearing NK cells.

An IL-2 immunocytokine has a greater efficacy relative to free IL-2. However, some characteristics of IL-2 immunocytokines may aggravate potential side effects of the IL-2 molecule. Because of the significantly longer circulating half-life of IL-2 immunocytokines in the bloodstream relative to free IL-2, the probability for IL-2 or other portions of the fusion protein molecule to activate components generally present in the vasculature is increased. The same concern applies to other fusion proteins that contain IL-2 fused to another moiety such as Fc or albumin, resulting in an extended half-life of IL-2 in circulation.

The invention provides altered IL-2 fusion proteins, such as IL-2 fused to an intact antibody or to a portion of an antibody, or to albumin, with reduced toxicity compared to unaltered forms of such fusion proteins. The invention also provides fusion proteins with one or more alterations in the IL-2 and/or the non-IL-2 moieties that alter the relative activity of the fusion protein in cells expressing the  $\alpha$ ,  $\beta$ , and  $\gamma$  IL-2 receptor subunits compared to cells expressing the  $\beta$  and  $\gamma$  IL-2 receptor subunits. The invention also provides for altered



IL-2 containing fusion proteins that exhibit an altered affinity towards the  $\alpha$ ,  $\beta$ , or  $\gamma$  subunit of the IL-2 receptor compared to unaltered forms of such fusion proteins.

A number of IL-2-containing antibody fusion proteins exhibit IL-2 activity that is quantitatively altered with respect to free IL-2, but is not qualitatively optimal for therapeutic applications. The invention provides modified forms of antibody-IL2 fusion proteins in which IL-2 or the antibody, or both moieties, are altered to qualitatively improve the IL-2 activity for a given application.

The invention also provides strategies for determining the types of modifications that are particularly useful in designing modified fusion proteins for treatment of diseases.

FIG. 1 illustrates possible mechanisms by which a fusion protein may bind to a cell surface, such that the receptor-binding properties of a moiety within the fusion protein are altered. For example, FIG. 1A depicts the fusion partner to IL-2 as a dimeric molecule. This increases the probability that the second IL-2 molecule interacts with its receptor, for example by decreasing the off-rate, which leads to a net increase in binding. FIG. 1B illustrates a second mechanism that produces the same effect. In cells that bear both a receptor for IL-2 and a receptor for the IL-2 fusion partner of the fusion protein (e.g. an Fc receptor for the Fc part of an Ig moiety) the receptor for the fusion partner (e.g. the Fc receptor) can engage the fusion protein and tether it at the cell surface where it now has an increased likelihood to bind to an IL-2 receptor.

A Phase I/II trial of an antibody-cytokine fusion protein, termed huKS-IL2, was recently completed. huKS-IL2 is a fusion protein consisting of the KS-1/4 antibody fused to the cytokine, interleukin-2. KS-1/4 recognizes the tumor cell surface antigen EpCAM (epithelial cell adhesion molecule) and has the effect of concentrating IL-2 at the tumor site. In the course of this trial, patient responses to treatment were measured. One patient who showed significant response to the therapy experienced a clinical partial response followed by disease stabilization and reduction in the use of pain medication. The patient had already received prior standard treatments that had failed. The patient's life was extended significantly beyond what was expected in the absence of such treatment.

Surprisingly, as a result of prior chemotherapy, this patient's T cell population was essentially obliterated. This patient had much lower T cell counts than all the other patients in the trial. Given that IL-2 is known to activate T cells and, for example, is known to enhance the cytotoxicity of CD8(+) T cells toward tumor cells, the strong response of this patient apparently lacking T cells was particularly unexpected. This observation prompted further study of novel antibody-IL-2 fusion proteins in which the IL-2 moiety might exhibit altered cell specificity, resulting in an improvement in the therapeutic index of IL-2 fusion proteins.

From the crystal structure of IL-2, sequence comparisons with related cytokines, and site-directed mutagenesis studies, much progress has been made in elucidating amino acids in IL-2 that come in contact with different IL-2 receptor subunits and their consequence on biological activity. For instance, the D20 residue, conserved in IL-2 across mammalian species, is a critical residue for binding the  $\beta$  subunit of the IL-2 receptor and various substitutions at this position have distinct effects. For example, the variant IL-2(D20K) fails to bind to any IL-2R complex and is generally inactive, while variants IL-2(D20E) or IL-2(D20T) retain their biological activity. Amino acid positions R38 and F42 are critical for binding the  $\alpha$  subunit, and while mutations at these sites diminish the interaction of IL-2 with the high affinity receptor

IL-2R $\alpha\beta\gamma$ , it still binds to the intermediate affinity receptor IL-2R $\beta\gamma$  and thus some bioactivity is retained. N88 is another residue that is involved in mediating interactions with the  $\beta$  subunit, and while the IL-2 (N88R) variant has greatly reduced affinity for the intermediate affinity receptor, its affinity for the high affinity receptor is essentially unchanged. The N88R mutant of IL-2 is therefore still able to activate T cells.

Binding affinity of fusion proteins of the invention for different receptors can be determined by a number of methods known in the art including, for example, a radioimmunoassay.

It is thus possible to perturb the IL-2 structure so that it displays greater affinity toward one IL-2 receptor complex compared with another IL-2 receptor complex by mutating a specific amino acid that contacts one of the receptor subunits, or by altering a combination of amino acid residues. As a consequence, the molecule displays greater activity in one cell type versus another. According to the invention, it is possible to manipulate the structure of IL-2 in the context of an Ig-IL2 fusion protein to obtain the desired effect. Moreover, in some instances, the Ig-IL2 variant fusion protein possesses different biological characteristics compared to the corresponding free IL-2 mutant protein.

It is furthermore possible, according to the invention, to manipulate the IL-2 moiety in a fusion protein so that it displays an altered affinity toward one or more of the IL-2 receptor subunits ( $\alpha$ ,  $\beta$ , or  $\gamma$ ) and results in an overall decrease in bioactivity of the fusion protein. Such variants are able to activate IL-2 responsive cells, but require a higher concentration than free IL-2. Accordingly, when IL-2 fusion proteins are concentrated at a desired target site, for example by a targeting moiety, these variants have an improved therapeutic index.

The  $\alpha$  receptor subunit of IL-2R appears to play a tethering function: this low-affinity receptor binds to IL-2 and keeps IL-2 close to the cell surface, so that the effective concentration in the neighborhood of cell surface IL-2R $\beta$  and IL-2R $\gamma$  receptor subunits is increased. Together, the  $\alpha$ -subunit and the  $\beta\gamma$ -subunits of the IL-2 receptor create the high affinity IL-2R complex. The invention is based, in part, on the recognition that IL-2 fusion proteins can engage in multiple and distinct interactions with receptors on the cell surface. For example, in the case of fusion proteins containing an antibody moiety, the antibody moiety itself may promote binding of the fusion protein to the cell surface and furthermore, IL-2 may be present in multiple copies in the fusion protein. As a result, IL-2 may be tethered to a cell expressing only the  $\beta$  and  $\gamma$  subunits of IL-2R, and have an enhanced ability to activate such a cell.

For example, a dimeric immunoglobulin (Ig) fused to IL-2 possesses two copies of IL-2, such that the binding of one IL-2 moiety to its receptor enhances the probability of an interaction of the second IL-2 moiety with a receptor molecule on the same cell surface. The diagram in FIG. 1A represents a possible configuration of an Ig-IL2 fusion protein on a cell surface. The invention provides Ig-IL2 fusion proteins in which the IL-2 moiety is altered to reduce binding to an IL-2R $\beta\gamma$  receptor.

A second mechanism by which Ig-IL2 fusion proteins may have altered binding to the surface of certain immune cells is that the Fc receptor on a cell surface may bind to the Fc part of an Ig moiety and thus tether the IL-2 to the surface of cells possessing both an Fc receptor and an IL-2 receptor (FIG. 1B). Such cells include NK cells, B cells, and macrophages. The invention provides Ig-IL2 fusion proteins in which the Ig moiety is altered to reduce binding to an Fc receptor. The invention further provides Ig-IL2 fusion proteins in which



both the Ig-moiety and the IL-2 moiety incorporate alterations of the nature described above.

Based on the insight that Ig-IL2 fusion proteins may be artificially tethered to cells bearing IL-2 receptor subunits, it is possible to design variant fusion proteins in which the tethering moiety is altered. For example, it is useful to alter the Fc-receptor binding features of an Ig-IL2 fusion protein. This may be done, for example, by mutating known amino acid contact sites within the Fc moiety or by removing the N-linked glycosylation sites, either by mutation or by enzymatic digestion of the protein.

Similarly, according to the invention it is useful to introduce mutations within the IL-2 moiety that have an effect on binding to IL-2 receptor subunits. In particular, it is useful to mutate amino acids in IL-2 that come into contact with the p subunit of IL-2 receptor. A particularly useful type of mutation is one that reduces the energy of binding between IL-2 and IL-2R $\beta$ , but does not sterically hinder this interaction. For example, mutation of a contact amino acid to an amino acid with a smaller side chain is particularly useful. The effect of such mutations is to reduce affinity of IL-2 for the  $\beta$ - $\gamma$  form of IL-2 receptor by a significant degree and also to reduce the activation of the signaling pathway mediated by these receptors, but to have relatively little or no effect on binding to the  $\alpha$ - $\beta$ - $\gamma$  form of the IL-2 receptor or on the activity elicited by IL-2 in cells bearing such IL-2 receptors. In a preferred embodiment of the invention, a mutation reduces the affinity for the  $\beta$ - $\gamma$  form of the IL-2 receptor, but does not eliminate it.

Similarly, it is useful to introduce mutations in amino acids on the surface of IL-2 that interact with the  $\alpha$  subunit of IL-2 receptor. A particularly useful type of mutation is one that reduces the energy of binding between IL-2 and IL-2R $\alpha$ , but does not sterically hinder this interaction. For example, mutation of a contact amino acid to an amino acid with a smaller side chain is particularly useful. The effect of such mutations is to reduce the affinity for the  $\alpha$ - $\beta$ - $\gamma$  form of IL-2 receptor to a significant extent, but to have relatively little or no effect on binding to the  $\beta$ - $\gamma$  form of the IL-2 receptor. In a preferred embodiment of the invention, a mutation reduces the affinity for the  $\alpha$ - $\beta$ - $\gamma$  form of the IL-2 receptor, but does not eliminate it.

Similarly, it is also useful to introduce mutations in amino acids on the surface of IL-2 that interact with the  $\gamma$  subunit of IL-2 receptor. As in the preceding cases, a particularly useful type of mutation reduces the energy of binding between IL-2 and IL-2R $\gamma$ , but does not sterically hinder this interaction. For example, mutation of a contact amino acid to an amino acid with a smaller side chain is particularly useful. The effect of such mutations is to reduce the affinity for the  $\beta$ - $\gamma$  form of IL-2 receptor to a significant extent, but to have relatively little or no effect on binding to the  $\alpha$ - $\beta$ - $\gamma$  form of the IL-2 receptor. In a preferred embodiment of the invention, a mutation reduces the affinity for the  $\beta$ - $\gamma$  form of the IL-2 receptor, but does not eliminate it.

It is also useful to introduce a combination of amino acid mutations into IL-2 that interact with different surfaces of the IL-2 receptor subunits. While each mutation independently may have little or no effect on binding of IL-2 to either the  $\alpha$ - $\beta$ - $\gamma$  or the  $\beta$ - $\gamma$  form of the IL-2 receptor, the combination of mutations may achieve the desired reduction in affinity of IL-2 for its receptor or the bioactivity of IL-2.

According to the invention, mutations in other parts of IL-2 indirectly contribute to alterations in the interaction of IL-2 with either the  $\beta$ - $\gamma$  form or the  $\alpha$ - $\beta$ - $\gamma$  form of the IL-2 receptor, and thereby result in an IL-2 molecule with modulated activity. For instance, a mutation may slightly alter the conformation of the molecule and alter its binding properties.

According to the invention, it is also useful to produce fusion proteins that contain mutations in the IL-2 moiety that modulate binding of the IL-2 moiety to an IL-2 receptor complex and also mutations in the antibody moiety. These fusion proteins may be particularly useful if it is desired to alter the interaction of the Ig-IL2 fusion protein with particular Fc receptors.

A free IL-2 moiety can display different binding characteristics for an IL-2R complex than when the IL-2 moiety is fused to another protein moiety such as an Ig. One possible mechanism by which this occurs is presented above. Another possible mechanism is that IL-2 is sterically or conformationally constrained in the context of the immunocytokine and that the particular constraint is reflected in the binding characteristics of the IL-2 moiety towards the different IL-2 receptor complexes. It is therefore useful to introduce alterations in the fusion protein that will modulate this constraint. For example, changes in the non-IL-2 moiety are useful in modulating the activity of IL-2.

The usefulness of a particular IL-2 fusion protein, such as an Ig-IL2 fusion or an IL-2 fusion protein containing Fc or albumin, for a particular application, such as treatment of human disease, is tested in an appropriate cellular or animal model. When possible, testing in an animal is preferred, because such testing comes closer to the full complexity of the behavior of the immune system in a human disease. For example, a particular balance of certain cells may be optimal to fight a disease of interest, such as cancer or an infection with a bacterium, virus, or parasite. For example, a relatively high level of T cell activity may be useful against a certain tumor type, while a relatively high level of NK cell activity may be useful against a different tumor type.

Another feature of the invention is IL-2 fusion protein variants, such as Ig-IL2 fusions or IL-2 fusions containing Fc or albumin, with superior toxicity profiles. For example, an Ig-IL2 fusion protein containing the mutation D20T shows reduced toxicity in animals such as mice as compared to corresponding Ig-IL2 fusion proteins with D at position 20. In another example, an Ig-IL2 fusion protein containing the mutation N88R or the combination of mutations L85T, 186T, N88R in the IL-2 moiety shows reduced toxicity in animals such as mice as compared to corresponding Ig-IL2 fusion proteins with N at position 88. In addition, an antibody-IL2 fusion protein containing the mutation D20T or the mutation N88R in the IL-2 moiety shows comparable potency to the corresponding parental antibody-IL2 fusion protein when used to treat a tumor that expresses an antigen target of the antibody.

The properties of the D20T variant of Ig-IL2 fusion proteins is particularly surprising in light of the reported properties of the D20T mutation in the free IL-2 protein. Specifically, the D20T mutation in the free IL-2 protein does not display a difference relative to the wild-type IL-2 protein in its activity towards IL-2R $\alpha$  $\beta$  $\gamma$ -bearing cells or IL2R- $\beta$  $\gamma$ -bearing cells (Shanafelt et al., PCT WO99/60128). However, an Ig-IL2 fusion protein containing the D20T mutation has a drastically reduced potency in activation of IL2R- $\beta$  $\gamma$ -bearing cells, but has essentially normal potency in activating IL-2R $\alpha$  $\beta$  $\gamma$ -bearing cells.

Accordingly, mutation of several amino acids within the IL-2 moiety of an Ig-IL2 fusion protein leads to reduced toxicity while having relatively little effect on the potency of the fusion protein in the treatment of various diseases. For instance, the extent to which the affinity of an IL-2 fusion protein variant for its receptors may be altered is a function of how well the particular fusion protein is concentrated at its intended target site. It is particularly useful to mutate one or



more of the following amino acids within the IL-2 moiety: Lys8, Gln13, Glu15, His16, Leu19, Asp20, Gln22, Met23, Asn26, Arg38, Phe42, Lys43, Thr51, His79, Leu80, Arg81, Asp84, Asn88, Val 91, Ile92, and Glu95. It is also useful to mutate one or more of the following amino acids within the IL-2 moiety: Leu25, Asn31, Leu40, Met46, Lys48, Lys49, Asp109, Glu110, Ala112, Thr113, Val115, Glu116, Asn119, Arg120, Ile122, Thr123, Gln126, Ser127, Ser130, and Thr131.

This invention discloses forms of an Ig moiety fused to IL-2, for example antibody-IL2 fusions such as huKS-IL2 or dI-NHS76-IL2, in which changes in the Ig moiety fused to IL-2 affect the binding properties of the fusion protein to the IL-2R complex. These changes may be amino acid substitutions in the amino acid sequence of the heavy chain, or chemical modifications. Useful amino acid substitutions include those that affect the glycosylation of the fusion protein or that directly affect interaction with an Fc receptor. A particularly useful substitution may be one that inhibits the glycosylation normally found at position N297 (EU nomenclature) of the IgG heavy chain. Chemical and biochemical modifications include PEGylation of the molecule or treatment with N-glycanase to remove N-linked glycosyl chains. Without wishing to be bound by theory, one may envisage that specific changes in the antibody portion of the molecule could affect the conformation of IL-2, for instance by altering the rigidity of the antibody molecule. In the case of huKS-IL2, these alterations may lead to a KS-IL2 molecule which now shows an increased selectivity towards T cells in a cell based bioassay.

For antibody-IL2 fusion proteins it is often useful to select an Ig moiety that confers other desired properties to the molecule. For example, an IgG moiety of the gamma 1 subclass may be preferred to maintain immunological effector functions such as ADCC. Alternatively, an IgG moiety of the gamma 2 or gamma 4 subclasses may be preferred, for example to reduce FcR receptor interactions. When using IgG moieties of subclasses gamma 2 or gamma 4, inclusion of a hinge region derived from gamma 1 is particularly preferred.

It is often useful to use the mutations and chemical or biochemical modifications of Ig-IL2 fusion proteins in combination with other mutations having distinct useful properties, such as the mutation of the lysine at the C-terminus of certain Fc regions to an alanine or another hydrophobic residue. For example, it is particularly useful to apply the modifications of the invention to the antibody fusion protein huKS-ala-IL2 or dI-NHS(76)-ala-IL2. It is also preferred to introduce further mutations into the molecule that eliminate potential T-cell epitopes. It is particularly preferred that these mutations do not substantially alter the desired properties of the molecule.

This invention further discloses forms of an Ig moiety fused to IL-2, for example an antibody-IL2 fusion such as huKS-IL2, in which a specific alteration in the amino acid sequence of IL-2, for example IL2(D20T) or IL2(N88R) changes the binding properties of the fusion protein to the IL-2R complex. The amino acid sequence of mature human IL-2 protein is depicted in SEQ ID NO: 3. The changes in binding properties are reflected in an increased selectivity towards T cells in a cell based bioassay. The particular mutation influences the degree of selectivity towards T cells. In addition, these changes result in a fusion molecule, for instance huKS-ala-IL2(D20T) or huKS-ala-IL2(N88R), with less toxic side effects when administered to mice systemically than, for instance huKS-ala-IL2. Also, these changes lead to a fusion protein, for instance huKS-ala-IL2(N88R), that is at least as efficacious as the normal huKS-L2 or huKS-ala-IL2 in tumor therapy in a number of mouse tumor models.

Because the immunological responses required to clear a tumor are manifold and also vary from tumor type to tumor type, it may not be desirable to completely eliminate a functionality from the molecule when a molecule with reduced toxicity is used. For instance, in a mouse model where pulmonary metastasis of colon carcinoma was induced, huKS-IL2 was shown to effectively treat the cancer by a T cell mediated mechanism, which did not require NK cells, whereas in a mouse model for neuroblastoma, the elimination of the tumor by huKS-IL2 was shown to require NK cells but not T cells. Therefore, there are cases where the selectivity profile may be more appropriately modulated to still allow an NK mediated response. In one embodiment of the invention, a more desirable approach is to subtly alter the selectivity profile of the molecule such that a response involving multiple receptor types is still achieved, most preferably at the sites where the molecule is concentrated. For example, the invention provides alterations of an Ig-IL2 fusion protein in which the selectivity for the IL-2R $\alpha\beta\gamma$ , relative to IL-2R $\beta\gamma$ , is enhanced 2- to 10-fold, 10- to 100-fold, 100- to 1000-fold, or more than 1000-fold, relative to a corresponding unmodified Ig-IL2 fusion protein.

Another object of the invention is to provide for optimal uses of Ig-IL2 fusion proteins with reduced toxicity for the treatment of cancer or infectious disease. While altered selectivity may lead to reduced vascular toxicity, it may not lead to optimal increases in the therapeutic index upon increasing the dose of the fusion protein. For example, these increases in dose may lead to an induction of negative regulatory mechanisms that regulate immune responses. It may therefore be useful to use treatment modalities that combine low-toxicity Ig-IL2 fusion proteins with agents that decrease such effects.

One recently identified potent inhibitor of cellular immune responses is a class of CD4<sup>+</sup>CD25<sup>+</sup> regulatory T cells that express the high affinity IL-2R (for a review, see Maloy and Powrie, (2001) *Nature Immunol.* 2:816). According to the invention, increased doses of low-toxicity Ig-IL2 fusion proteins may additionally activate these cells. Upon stimulation, these cells up-regulate CTLA-4 on their cell surface, which engage cell surface molecules B7-1 and B7-2 on immune cells and in turn elicit a potent negative signal (Takahashi et al., (2000) *J. Exp. Med.* 192: 303). Thus, inhibitors of these processes could be useful in combination therapy with fusion proteins of the invention. In one embodiment, antibodies neutralizing CTLA-4 and its effects can be used. In another embodiment, other proteins with similar activity can be used, such as soluble B7 receptors and their fusion proteins (e.g. B7-Ig). Further embodiments include the use of antibodies that kill or inhibit these regulatory T cells themselves such as anti-CD4 and anti-CD25. In a preferred embodiment, the latter are administered sequentially rather than simultaneously.

According to the invention, another useful mechanism involves overstimulation of cyclo-oxygenase 2 (COX-2) leading to the production of prostaglandins, which are known to inhibit immune responses (see PCT US99/08376). Therefore, a further embodiment combines the use of the low-toxicity Ig-IL2 molecules with COX-2 inhibitors such as Indomethacin, or the more specific inhibitors Celecoxib (Pfizer) and Rofecoxib (Merck&Co). It is understood that still other immune mechanisms might be activated by increasing doses of low-toxicity Ig-IL2 fusion proteins and that combination therapies may be devised to address these mechanisms. In addition, low doses of certain cytotoxic drugs, such as cyclophosphamide, which have immune potentiating effects in vivo may be useful therapeutic agents to include in a combination therapy.



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Fusions of albumin have been developed with the purpose of generating therapeutic fusion proteins with enhanced serum half-lives. For example, Yeh et al. (Yeh P, et al. Proc Natl Acad Sci USA. [1992] 89:1904-8.) constructed an albumin-CD4 fusion protein that had a much longer serum half-life than the corresponding CD4 moiety alone.

It is useful to construct fusions of albumin to IL-2, erythropoietin, interferon-alpha, and other ligands. These fusion proteins have longer serum half-lives than the corresponding ligand alone. Such fusions may be constructed, in the N- to C-terminal direction, as ligand-albumin fusions or albumin-ligand fusions, using standard genetic engineering and protein expression techniques. Alternatively, albumin and a ligand may be joined by chemical conjugation.

However, albumin-ligand fusion proteins often have undesirable properties. Without wishing to be bound by theory, one reason for why albumin-ligand fusion proteins may have undesirable properties is the fact that there are receptors for albumin on vascular endothelial cells (Tiruppathi et al. Proc Natl Acad Sci USA. [1996] 93:250-4). As a result, the effects of a ligand on vascular endothelial cells may be enhanced.

For example, an albumin-IL2 fusion protein has an enhanced serum half-life, but also causes enhanced vascular leak. Without wishing to be bound by theory, it is noted that activation of IL-2 mediated responses in the vasculature is increased because of binding of the fusion protein to albumin receptors present on endothelial cells of the vasculature. Binding of albumin-IL2 fusion proteins to cells that have receptors both for albumin and IL-2 is enhanced by a mechanism analogous to that shown in FIG. 1b for the enhancement of binding of an Ig-ligand fusion protein to a cell surface.

To reduce the vascular leak caused by albumin-IL2, it is useful to introduce mutations into the IL-2 moiety that specifically reduce IL-2's affinity for IL-2R $\beta\gamma$  receptors. For example, an albumin-IL2(N88R) or albumin-IL2(D20T) fusion protein is constructed and subsequently found to have reduced toxicity and an enhanced therapeutic index for a disease model in an animal such as a mouse.

Molecules of the present invention are useful for the treatment of malignancies and tumors, particularly treatment of solid tumors. Examples of tumors that can be treated according to the invention are tumors of epithelial origin such as those present in, but not limited to, ovarian cancer, prostate cancer, stomach cancer, hepatic cancer, bladder, head and neck cancer. Equally, according to the invention, malignancies and tumors of neuroectodermal origin are suitable candidates for treatment, such as, but not limited to, melanoma, small cell lung carcinoma, soft tissue sarcomas and neuroblastomas.

According to the invention, it is useful for the therapeutic agent to be targeted to the tumor site or the site of the malignancy or metastasis. Ig-fusion proteins containing antibodies directed toward antigens preferentially presented by tumors or malignant cells are particularly useful. For example, fusion proteins containing an antibody moiety with specificity for EpCAM (eg KS1/4), or embryonic Fibronectin (eg. BC1), or CEA, or chromatin complexes (eg. NHS76), or GD2 (eg 14.18), or CD19, or CD20, or CD52, or HER2/neu/c-erbB-2, or MUC-1, or PSMA are particularly useful. In addition, antibodies directed to various viral antigens are particularly useful.

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## EXAMPLES

## Example 1

### Construction of Ig-IL2 Fusion Genes with Codon Substitutions in the IL-2 Coding Sequence or in the Antibody Coding Sequence

An expression vector for immunocytokines was described in Gillies et al., (1998) J. Immunol. 160:6195-6203. Several modifications in the nucleotide sequence enabled the addition of coding sequences to the 3' end of the human  $\gamma$ -1 gene. In the human  $\gamma$ -1 gene encoding the heavy chain, the XmaI restriction site located 280 bp upstream of the translation stop codon was destroyed by introducing a silent mutation (TCC to TCA). Another silent mutation (TCT to TCC) was introduced to the Ser codon three residues upstream of the C-terminal lysine of the heavy chain to create the sequence TCC CCG GGT AAA (SEQ ID NO. 4), which contains a new XmaI site [Lo et al., (1998) Protein Engineering 11:495-500].

The IL-2 cDNA was constructed by chemical synthesis and it contains a new and unique PvuII restriction site [Gillies et al., (1992) Proc. Natl. Acad. Sci. 89:1428-1432]. Both the XmaI and PvuII sites are unique in the expression vector, and they facilitated construction of antibody-IL2 variants, including the following.

1) huKS-ala-IL2. The construction of huKS-ala-IL2 has been described previously (e.g. WO01/58957). The resulting protein contains an amino acid substitution at the junction between the Ig heavy chain constant region and mature huIL-2. The junction normally has the sequence SPGK-APT (SEQ ID NO: 5) in which -SPGK- is the C-terminus of the heavy chain and -APT- the N-terminus of the mature IL-2 protein. In huKS-ala-IL2 a K to A substitution was introduced (referred to as position K[-1]) and the junction now has the sequence SPGA-APT (SEQ ID NO: 6). As a consequence the serum half-life of this protein is improved (see Example 5).

2) dI-KS-ala-IL2. This KS-IL2 fusion protein contains substitutions in KS-ala-IL2 to generate a version of the fusion protein in which potential T-cell epitopes have been eliminated (described in co-pending patent applications U.S. Ser. Nos. 10/112,582 and 10/138,727, the entire disclosures of which are incorporated by reference herein).

The constant region of the Ig portion of the fusion proteins of the invention may be selected from the constant region normally associated with the variable region, or a different constant region resulting in a fusion protein with the Ig portion including variable and constant regions from different subclasses of IgG molecules or different species. For example, the gamma4 constant region of IgG (SEQ ID NO: 7) may be used instead of gamma1 constant region (SEQ ID NO: 8). The alteration has the advantage that the gamma4 chain can result in a longer serum half-life. Accordingly, IgG gamma2 constant region (SEQ ID NO: 9) may also be used instead of IgG gamma1 constant region (SEQ ID NO: 8). In addition, the hinge region derived from IgG gamma1 (SEQ ID NO: 10) may replace the hinge region normally occurring in IgG gamma2 (SEQ ID NO: 11) or IgG gamma4 constant region (SEQ ID NO: 12). The Ig component of the fusion protein may also include mutations in the constant region such that the IgG has reduced binding affinity for at least one of Fc $\gamma$ RI, Fc $\gamma$ RII or Fc $\gamma$ RIII. The fusion proteins of the invention may include mutations in the IgG constant regions to remove potential glycosylation sites and T-cell epitopes. For example, the various constant regions may include alterations in the C-terminal part of the constant regions to remove potential T-cell epitopes. For example, potential T-cell epitopes in



the C-terminal part of various constant regions of IgG molecules are removed by changing the amino acid sequence KSLSLSPGK (SEQ ID NO: 13) in IgG gamma1 and IgG gamma 2 constant regions and amino acid sequence KSLSLSLGK (SEQ ID NO: 14) in IgG gamma4 constant region to amino acid sequence KSATATPGA (SEQ ID NO: 15).

3) huKS-ala-IL2(N88R). This huKS-IL2 variant contains the same amino acid substitution at the junction between the Ig heavy chain constant region and mature huIL-2 as described above (K[-1]A, created by the codon change AAA to GCC), and in addition it contains a substitution at position N88 in the sequence of mature huIL-2 in favor of R (created by codon change aAT to aGG). A further alteration was introduced into the nucleotide sequence of huIL-2 to eliminate an existing restriction site for Bam HI by introducing a silent mutation (amino acid position G98, the codon was switched from ggA tcc to ggC tcc).

A PCR-based mutagenesis strategy was used in the construction of huKS-ala-IL2(N88R). Two overlapping PCR fragments that span the coding sequence of the mature huIL2 were generated using huIL2 in a Bluescript vector (Stratagene) as a template. The upstream PCR fragment contained the nucleotide changes encoding K[-1]A and N88R by incorporating these mutations into the sense and antisense primers respectively. These changes are indicated by the bold nucleotides in the primer sequences. The sense primer sequence was: 5'CCCCGGGTGCCGCCCAACTTCAAGTTC-TACA3'(SEQ ID NO: 16); the antisense primer sequence was: 5'AGCCCTTTAGTTCCAGAACTATTACGTTGATC-CTGCTG ATTAAGTCCCTAGGT 3'. (SEQ ID NO: 17). The underlined nucleotide represents a change that destroys the Bam HI site. The second, downstream PCR fragment contained a 20 nucleotide overlap region with the upstream PCR fragment and the remaining IL2 sequence. The sense primer used in this reaction was 5'AGTTCTGGAACTAAAGGGCTCCGAAACAACATTCATGTGT (SEQ ID NO: 18). Again, the underlined nucleotide denotes the silent mutation that destroys the Bam HI site. The antisense primer used was the standard M13 reverse primer that anneals to a sequence in the pBluescript vector. These overlapping PCR fragments were used in a reaction with the primer in SEQ ID 16 and an M13 reverse primer to generate the final PCR product, which was subsequently inserted into a TA vector (Invitrogen).

The sequence of the inserted fragment was verified, and a 442 bp Xma I/Xho I fragment containing the modified IL2 sequence (from plasmid TA-IL2(N88R)) was used to replace the wild-type huIL-2 sequence in the parental immunocytokine expression plasmid (encoding huKS-IL2). The resultant immunocytokine expression plasmid encoding huKS-ala-IL2(N88R) was verified by restriction mapping and sequencing.

4) huKS M1-IL2(TTSR (SEQ ID NO: 19)). The immunocytokine variant huKS M1-IL2 was constructed by standard recombinant DNA techniques (and described e.g. in co-pending patent application U.S. Ser. No. 10/112,582, the entire disclosure of which is incorporated by reference herein). It contains multiple amino acid substitutions in the antibody-IL-2 junction region of the fusion protein, which eliminate potential T-cell epitopes and results in a less immunogenic protein. The sequence was changed from KSLSLSPGA-APT (SEQ ID NO: 20) to KSATATPGA-APT (SEQ ID NO: 21) (the dash denotes the Ig/IL-2 junction site and substituted amino acids are underlined) and is denoted as "M1". Also incorporated in this variant is the K to A change at the last

amino acid before the junction that has been shown to increase serum half-life of the immunocytokine.

huKS M1-IL2(TTSR) contains further amino acid substitutions located in the IL-2 portion of the immunocytokine. To eliminate potential T-cell epitopes created by the substitution of N88R described above, the sequence is changed from -D LISNI- (SEQ ID NO: 22) of the natural huIL-2 to -DTTSRI- (SEQ ID NO: 23).

A PCR based mutagenesis approach was used to introduce the changes into the nucleotide sequence of the huIL-2 gene, by incorporating the mutations into the sense primer. The sequence TTxR was created by codon changes ACC, ACC and AGG respectively. A mutagenized 197 bp PCR fragment encompassing the 3' end of the hu IL-2 sequence was generated from the template immunocytokine expression plasmid encoding huKS-ala-IL2(N88R) using a sense primer of the sequence 5'ACTTAAGACCTAGGGACACCACCAGCAG-GATCAACGTAATAGT3' (SEQ ID NO: 24) and an antisense primer of the sequence 5'ATCATGTCTGGATCCCTC3' (SEQ ID NO: 25). The PCR fragment was cloned into a TA vector and the sequence verified. To regenerate the complete IL-2 sequence this fragment was ligated as a Afl II/Xho I restriction digest to a 2 kb Hind III/Afl II fragment obtained from immunocytokine expression plasmid encoding huKS-ala-IL2(N88R) and inserted into a Hind III/Xho I restricted pBluescript vector. The mutagenized IL-2 gene was then exchanged in place of the natural huIL-2 sequence in an immunocytokine expression plasmid encoding for KS M1-IL2 in a three-way ligation.

5) huKS(N to Q)-IL2. An immunocytokine expression plasmid encoding huKS(N to Q)-IL2 was constructed using standard recombinant DNA techniques. huKS(N to Q)-IL2 contains an amino acid substitution in the CH2 domain of the antibody Fc gamma 1 constant region that eliminates N-linked glycosylation. The amino acid sequence is changed from QYNSTYR (SEQ ID NO: 1) to QYQSTYR (SEQ ID NO: 26), with the substituted amino acid indicated in bold. Similarly, fusion proteins including gamma 2 and gamma 4 constant regions were constructed that contain mutations that change the amino acid sequence QFNST (SEQ ID NO: 2) to QAQST (SEQ ID NO: 27), thereby additionally eliminating a potential T cell epitope.

## Example 2

### Chemical or Enzymatic Modifications of an Ig-IL2 Fusion Protein Leading to Modified Receptor Specificity

This example describes biochemical manipulations of the immunocytokine used to generate a PEGylated huKS-IL2 or to a deglycosylated huKS-IL2, and variants thereof. The same methods can be applied to other IL-2 fusion proteins, such as the immunocytokine 14.18-IL2 or albumin-cytokine fusions. These variants were used in a subsequent example to investigate their effect on the proliferative response of various cell lines in a cell based bioassay (Table 1) or on the pharmacokinetic properties of the molecule.

PEGylation of huKS-IL2. PEG (20,000) was covalently attached to the protein via amine groups present on the protein. For this purpose a reactive derivative of PEG containing a succinimide linker (mPEG-Succinimidyl Propionate, termed "SPA-PEG" below) was employed. huKS-IL2 was extensively dialyzed in an amine-free buffer composed of 50 mM Sodium Phosphate (pH 7.5), 0.05% Tween 80, and concentrated. Excess SPA-PEG was combined with huKS-IL2 at a molar ratio of either 5:1 or 10:1. Immediately before use, a



5 mM SPA-PEG stock solution was prepared in deionized water. An appropriate volume of the SPA-PEG solution was combined with huKS-IL-2 and the reaction was incubated on a rocking platform for 30 to 40 minutes at room temperature. A 5 to 10 molar excess of glycine was added to quench the reaction, and the reaction products were purified by size exclusion chromatography. A Superdex 200 column, equilibrated in 50 mM HEPES and 150 mM NaCl, was loaded with the reaction sample and eluting fractions containing the PEGylated protein were pooled and concentrated.

N-Glycanase treatment of huKS-IL2. huKS-IL2 (1.5 mg) was incubated with 30 mU PNGaseF (New England Biolabs) overnight at 37° C. The reaction product was purified by passage over a ProteinA-Sepharose column and elution of the bound huKS-IL2 at pH 3. The eluate was neutralized and concentrated in a spin column in a buffer of PBS and 0.05% Tween80. Deglycosylation of huKS-IL2 was verified by size exclusion chromatography and on a urea gel.

### Example 3

#### Expression and Purification of Ig-IL2 and Ig-IL2 Variants

The general procedure described here for huKS-ala-IL2 (N88R) may be used for a wide variety of Ig-cytokine fusion proteins, including Ig-fusions to mutant cytokines. To obtain stably transfected clones which express huKS-ala-IL2 (N88R), DNA of the immunocytokine expression plasmid encoding huKS-ala-IL2(N88R) was introduced into the mouse myeloma NS/0 cells by electroporation. NS/0 cells were grown in Dulbecco's modified Eagle's medium supplemented with 10% heat-inactivated fetal bovine serum, 2 mM glutamine and penicillin/streptomycin. About  $5 \times 10^6$  cells were washed once with PBS and resuspended in 0.5 ml PBS. 10  $\mu$ g of linearized plasmid DNA were then incubated with the cells in a Gene Pulser Cuvette (0.4 cm electrode gap, BioRad) on ice for 10 min. Electroporation was performed using a Gene Pulser (BioRad, Hercules, Calif.) with settings at 0.25 V and 500  $\mu$ F. Cells were allowed to recover for 10 min on ice, after which they were resuspended in growth medium and plated onto two 96 well plates. Stably transfected clones were selected by growth in the presence of 100 nM methotrexate (MTX), which was added to the growth medium two days post-transfection. The cells were fed every 3 days for two to three more times, and MTX-resistant clones appeared in 2 to 3 weeks. Supernatants from clones were assayed by anti-Fc ELISA to identify high producers. High producing clones were isolated and propagated in growth medium containing 100 nM MTX.

The immunocytokine was purified from the tissue culture supernatant by Protein A affinity column chromatography. For huKS-ala-IL2(N88R), a recombinant Protein A (rPA) Agarose column was pre-equilibrated with ten volumes of running buffer, such as 100 mM Arginine, 5 mM Citrate, 0.01% Tween 80 pH 5.6, and the column was loaded with filtered cell culture supernatant containing huKS-ala-IL2 (N88R) at 16 ml/min to a binding of approximately 40 mg/ml of rPA resin. The column was washed extensively with the same buffer and finally the immunocytokine was eluted in 50 mM glycine at pH 3. Peak fractions were collected and pH was adjusted to neutral with 1 N NaOH.

### Example 4

#### Activity of Ig-IL2 Variants in Bioassays

For cell based bioassays, cell lines that depend on IL-2 for growth were utilized and the activity of Ig-fusion proteins, for example huKS-IL2 and huKS-IL2 variants, was assessed by proliferation of these cells. For instance, CTLL-2 (ATCC# TIB-214; Matesanz and Alcina, 1996) and TF-1 $\beta$  (Framer et al., [1995] Blood 86:4568-4578) were used to follow a T cell response and an NK cell-like response, respectively. CTLL-2 is a murine T lymphoblast cell line that expresses the high affinity IL-2R $\alpha\beta\gamma$ , and TF-1  $\beta$  is a human cell line derived from immature precursor erythroid cells that express the intermediate affinity IL-2R $\beta\gamma$ . Another useful cell line for these assays is, for example, the cell line derived from human adult T cell lymphoma Kit-225 (K6) (Uchida et al., [1987] Blood 70:1069-1072). When paired with cell line TF-1 $\beta$ , the activity of the fusion proteins is evaluated in a pair of cell lines harboring receptors of the same mammalian species. These assays may also be performed with cell populations derived from human PBMCs (Peripheral Blood Mononuclear Cells), either to isolate NK-cells, which bear IL-2R $\beta\gamma$ , or to produce activated T cells, which express IL-2R $\alpha\beta\gamma$ . Techniques to isolate these cell populations from hu PBMCs are known to those of ordinary skill in the art. For example, T cells, or PHA-blasts, are obtained by incubating PBMCs for three days in 10 microgram/ml of phytohemagglutinin (PHA-P; L9017, Sigma, St. Louis). Resting NK cells are commonly obtained by a negative selection protocol, for instance using an NK-cell isolation kit (Miltenyi Biotec, Auburn, Calif.) for human cells. To correlate the activity of these fusion proteins with results obtained from mouse tumor models, it is also useful to perform these assays on cell populations obtained from the mouse expressing one or the other IL-2 receptor complex. For example, an NK cell population may be obtained from spleens of recombinant-deficient (SCID) Balb/C mice using a SPINSEPT<sup>TM</sup> murine NK-cell enrichment kit (Stemcell Technologies Inc, Vancouver, BC, Canada). The purity of any of these enriched populations can be assessed by FACS analysis.

Briefly, washed cells were plated at a density of 10,000 cells/well in a 96 well microtiter plate and incubated in cell medium supplemented with, for example, purified huKS-IL2 or huKS-IL2 variants. In addition, wild type huIL-2 protein, obtained from R&D Systems (Minneapolis, Minn.) was assayed as a standard. The added protein was prepared as a dilution series over a roughly 1000-fold concentration range between 0.45 ng/ml and 420 ng/ml (normalized with respect to molar equivalents of IL2). After 32 hours, 0.3  $\mu$ Ci of [methyl-3H]thymidine (Dupont-NEN-027) was added to each well and cells were incubated an additional 16 hours. Cells were then harvested and lysed onto glass filters. 3H-thymidine incorporated into DNA was measured in a scintillation counter.

An ED50 value for each huKS-IL2 protein variant with respect to cell proliferation was obtained from plotting a dose response curve and identifying the protein concentration that resulted in half-maximal response. The selectivity of the response was expressed as a ratio of ED50 values for example, ED50 [TF1- $\beta$ ]/ED50 [CTLL-2]. Thus, a high ED50 ratio indicated that a relatively higher dose of the protein was required to elicit a TF-1 $\beta$  cell response as compared to a CTLL-2 cell response. The ratio of the ED50 values of the



huKS-IL2 variants was compared to free huIL-2 and the parental huKS-IL2 proteins. This normalized value is a measure of the differential effect. A value larger than the one obtained for the reference protein indicated a shift in selectivity toward CTLL-2 cells. In some cases it may be preferable to obtain ED50 ratios with cell lines that originate from the same species, so that IL-2 activities are not additionally influenced by cross-species differences in their interaction with the receptors. The following example uses murine CTLL-2 and human TF-1 $\beta$  cells to calculate ED50 ratios with Ig-IL2 fusion proteins and free IL-2, and representative results from such an experiment are shown in Table 1.

TABLE 1

Protein	ED50 Ratio
IL-2	0.81
HuKS-IL2	0.11
HuKS-ala-IL2	0.17
KS(NtoQ)-IL2	0.72
HuKS-ala-IL2(N88R)	2300
KS-IL2(TTSR)	>6
HuKS-IL2 PEGylated	1.99
HuKS-IL2 + Glycanase	0.45
14.18-IL2	0.07
14.18-IL2 PEGylated	1.34
14.18-IL2 + Glycanase	0.21

In this example, compared with the ED50 ratio obtained with free IL-2 (0.81), an approximately 5-fold lower ED50 ratio was obtained with huKS-IL2 (0.17). This indicated that the fusion protein was shifted in its selectivity profile, displaying a greater selectivity towards TF-1 $\beta$  cells. A different antibody/IL-2 combination, 14.18-IL2, also was more selective for TF-1 $\beta$  than IL-2 alone (ED50 ratio of 0.07), indicating that this effect was not limited to a specific antibody contained in the antibody-IL2 fusion protein, and the reduced activity of human Ig-IL2 fusion proteins towards murine high affinity receptor bearing cells relative to huIL-2 may reflect a general feature of the Ig-IL2 fusion proteins.

Other variants had an altered ED50 ratio such that a CTLL-2 cell response was favored. A dramatic effect was seen with huKS-ala-IL2(N88R), for which the ED50 ratio was greater than 2000, reflecting that TF-1 $\beta$  cell proliferation, mediated in these cells by the intermediate affinity receptor, was barely detectable. Thus, while huKS-ala-IL2(N88R) activated signaling of cells with IL-2R $\alpha\beta\gamma$ , it did not significantly activate cells with IL-2R $\beta\gamma$ . The activity of huKS-ala-IL2(N88R) could also be assayed on purified murine NK cells expressing the murine IL-2R $\beta\gamma$  complex; in contrast to what was reported for the free human IL2(N88R) protein—which indicated that the selectivity was virtually lost when mouse T and NK cells were examined (see Wetzel et al., ASCO 2001 Meeting Abstract)—the ED50 value for huKS-ala-IL2 (N88R) in the mouse NK cells was similar to that observed with TF-1 $\beta$  cells.

Subtle shifts in the selectivity of the response towards CTLL-2 cells were observed in Ig-IL2 variants with alterations that affect glycosylation of the antibody portion of the fusion protein. Specifically, KS(NtoQ)-IL2, which lacks a glycosylation site in the Fc portion of the antibody, displayed a 3-fold increase in ED50 Ratio (0.72) relative to huKS-IL2, whereas N-Glycanase treated huKS-IL2 displayed a 2-fold increase (ED50 ratio of 0.45) relative to huKS-IL2. Likewise, N-Glycanase treatment of IL-2 fused to a different antibody molecule lead to a similar result; for instance, N-Glycanase treated 14.18-IL2 gave a 3-fold increase in the ED50 ratio as compared to untreated 14.18-IL2. These results indicated that

certain alterations in the antibody portion of the molecule itself affect the binding and activation properties of an IL-2 molecule fused to it.

PEGylation of the fusion protein also altered its selectivity profile. Again, a shift towards CTLL-2 stimulatory activity was observed. For huKS-IL2, a PEGylated variant resulted in a 9-fold increase in selectivity in favor of CTLL-2 cells (ED50 ratio of 1.99), and for 14.18-IL2 a 20-fold increase was induced by PEGylation (ED50 ratio of 1.34).

In some instances, these shifts in selectivity for a given protein may also reflect the particular combination of cell types employed in the assays, as illustrated in representative results shown in Table 2. For example, when KS-IL2, KS-ala-IL2 and IL-2 were compared using the human IL-2R $\alpha\beta\gamma$  bearing cell line Kit 225 instead of murine CTLL-2, the patterns of shift in selectivity was not maintained. Particularly with regards to Kit 225 cells, these three proteins exhibited essentially identical activity. Mostly however, the trends in the selectivity response of Ig-IL2 variants between TF-1 $\beta$  cells and Kit-225 cells were found to be similar to those established with TF-1 $\beta$  cells and CTLL-2 cells, including the effect of deglycosylation of the Fc-moiety of a Ig-IL2 fusion protein (see representative results in Table 2 below and Example 10).

TABLE 2

Protein	ED50 Ratio TF-1 $\beta$ /Kit-225
IL-2	2.8
HuKS-IL2	4
HuKS-ala-IL2	10.4
KS-ala-IL2(N88R)	52,000

In addition, it was found that Kit-225 cells were more sensitive to IL-2 and IL-2 fusion proteins and variants thereof than CTLL-2 cells. For example, the ED50 value for huKS-ala-IL2 was 0.08 in Kit-225 cells and 5.0 in CTLL-2 cells, and for KS-ala-IL2(N88R) it was 0.13 in Kit 225 cells and 3 in CTLL-2 cells, indicating an approximately 10-50 fold increase in sensitivity of Kit 225 cells in these assays. Thus the value of the ED50 ratio for a given protein is dependent on the particular combination of cell types employed.

### Example 5

#### Pharmacokinetics of IL-2 Fusion Proteins with Modified Receptor Binding Characteristics

The pharmacokinetic (PK) profile of huKS-ala-IL2(N88R) was compared to the profile of huKS-ala-IL2 and huKS-IL2. For each protein, three 6-8 week old mice were used. Twenty five  $\mu$ g of the fusion proteins, diluted to 125  $\mu$ g/ml in PBS, were injected in the tail vein of mice, and 50  $\mu$ l blood samples were obtained by retro-orbital bleeding immediately after injection (0 hrs) and at 0.5, 1, 2, 4, 8, and 24 hrs post injection. Blood samples were collected in heparin-coated tubes to prevent blood clotting, and immunocytokine levels in the post-cellular plasma supernatant were measured in an ELISA assay. The procedure of the ELISA assay used for pharmacokinetic studies has been previously described (WO01/58957). This assay measured the presence of an intact immunocytokine. Capture of the immunocytokine from plasma was carried out on EpCAM-coated plates and the detection was performed with an HRP-conjugated antibody directed against IL-2. It had been shown previously that the huKS-IL2 variant with a K to A substitution in the junction, huKS-ala-IL2, had



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a dramatic improvement in circulating half-life as compared to huKS-IL2 (WO01/58957). In fact, the circulating half-life of huKS-ala-IL2(N88R) was found to be similarly improved, indicating that the N88R alteration in the IL-2 portion of the molecule had no substantial effect on the pharmacokinetics. Results of a representative experiment are shown in FIG. 2. FIG. 2 illustrates a time course of the concentration of the immunocytokine present in the serum (expressed as a percentage of the protein concentration remaining in the serum relative to the starting concentration present immediately after intravenous administration) over 24 hours. Protein concentrations are determined in an ELISA assay in which the immunocytokine is captured by its antibody moiety and detected by its cytokine moiety. X-axis=time t in hours; Y-axis=log(% of remaining protein concentration).

## Example 6

## Toxicity of Ig-IL2 Fusion Proteins with Modified Receptor Binding Characteristics in a Mammal

The relative toxicity of the KS-IL2 variants huKS-IL2, huKS-ala-IL2, and huKS-ala-IL2(N88R) in mice was examined. As was shown in Example 5, huKS-ala-IL2 and huKS-ala-IL2(N88R) have substantially increased PK when compared to huKS-IL2. Nonetheless, for comparison purposes, an identical dosing schedule was used for the different molecules despite the difference in PK. While a longer serum half-life is likely to increase the efficacy of a therapeutic it may also lead to increased toxicity. Yet this example shows that, while huKS-ala-IL2 had increased toxicity compared to huKS-IL2 (because of a longer circulating half-life), huKS-ala-IL2(N88R) had decreased toxicity compared to huKS-IL2 despite a longer circulating half-life.

Balb/C mice (3 animals per experimental condition) were given daily intravenous injections of one of three proteins for five consecutive days. The fusion proteins were diluted into 200  $\mu$ l of PBS and were administered at the following dosage: huKS-IL2 and huKS-ala-IL2 at 25, 50, or 75  $\mu$ g per mouse, and huKS-ala-IL2(N88R) at 50, 75, or 100  $\mu$ g per mouse. A control group received intravenous injections of PBS. Survival of the mice was monitored daily and the effect on mouse survival was examined. Mice survived administration of all doses of huKS-IL2. huKS-ala-IL2, however, was more toxic. While the mice tolerated a dose of 25  $\mu$ g of huKS-ala-IL2, all 3 mice died on day 6 at a dose of 50  $\mu$ g, and at a dose of 75  $\mu$ g, two mice had died at day 4.5, and the third mouse at day 5. huKS-ala-IL2(N88R), on the other hand, was well tolerated at all doses, including 100  $\mu$ g. Indeed, huKS-ala-IL2(N88R) was also administered at a dose of 200  $\mu$ g per mouse, and the mice survived. Thus, huKS-ala-IL2(N88R) was significantly less toxic than huKS-ala-IL2.

Mice that had died during the course of the treatment with huKS-ala-IL2 were dissected and their organs evaluated. All organs, including lung, spleen, liver, stomach, and kidney were grossly distended, indicative of extensive vascular leakage. Organs of animals treated with variant huKS-ala-IL2 (N88R) were also evaluated. Mice were treated as described above, and it was found that organ weights from huKS-ala-IL2(N88R)-treated animals were generally similar to those of control animals, particularly for the lungs and liver. Without wishing to be bound by theory, it is thought that the increase in the weight of the spleen is more due to an increase in cellularity caused by an antibody immune response against this human protein rather than a vascular leak. It is inferred that huKS-ala-IL2(N88R) produces less severe vascular leaks

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than huKS-ala-IL2. Table 3 provides an example of approximate values for the x-fold increase in organ weight relative to organs of a control mouse:

TABLE 3

ORGAN	WEIGHT INCREASE (x fold)	
	HuKS-ala-IL2 (20 $\mu$ g/mouse)	huKS-ala-IL2(N88R) (100 $\mu$ g/mouse)
Lung	4	1.7
Spleen	3	3
Liver	1.5	1
Kidney	1	1

The effect of various mouse strain backgrounds, with known alterations in their immune system make-up, was evaluated with respect to the toxicity of these Ig-IL2 fusion proteins. Mouse strains DBA/2, Balb/C, B6.CB17-Prkdc<sup>scid</sup>/SzJ (SCID), beige, and SCID/beige were used. The fusion proteins were administered as above at a dose of 25  $\mu$ g and 50  $\mu$ g per mouse for huKS-ala-IL2 and at a dose of 200  $\mu$ g per mouse for huKS-ala-IL2(N88R), and mouse survival and weight was assessed over a two week period.

In the case of huKS-ala-IL2, most mice strains gave results similar to those seen with Balb/C mice reported above: the dose of 50  $\mu$ g led to animal death at day 5, whereas at the lower dose the animals survived and their weights recovered to about their initial weight but did not reach the weight gains of the mock-treated control animals. Interestingly, beige mice, deficient in functional NK cells, were better able to tolerate the high dose of 50  $\mu$ g; two animals had died by day 9, but one, while it initially lost significant weight (around 25% by day 7), recovered, and by day 15 had attained the body weight of mock-treated animals and those treated at the lower dose. DBA/2 mice were more sensitive to huKS-ala-IL2; even at the lower dose, DBA/2 animals died at day 5 and day 9.

With huKS-ala-IL2(N88R), the increased susceptibility of DBA/2 mice to Ig-IL2 fusion proteins was also apparent: by day 8, all animals had died, and even at half the dose (100  $\mu$ g) the animals had died by day 9. Again, the fusion protein was best tolerated in beige mice, whereas the SCID/beige mice lost significant weight (remained stable at around 80% of mock-treated control by day 10).

## Example 7

## Efficacy of an Ig-IL2 Fusion Protein with Modified Receptor Binding Characteristics in Treatment of Various Tumors in a Mammal

a) Treatment of a CT26/KSA subcutaneous tumor in Balb/C mice. CT26 colon carcinoma cells, transduced with the gene encoding human KS antigen (KSA), were used to induce a subcutaneous tumor.  $2 \times 10^6$  viable cells were suspended in 100  $\mu$ l of PBS and injected subcutaneously into the dorsa of 6 week old Balb/C mice. When tumor size reached 100-200  $\text{mm}^3$ , groups of 8 mice were subjected to one of three treatment conditions: on five consecutive days, intravenous injections with 15  $\mu$ g of either huKS-ala-IL2 or of huKS-ala-IL2(N88R) diluted into 200  $\mu$ l of PBS, or PBS alone, were administered. Disease progression was evaluated by measuring tumor volume twice a week for 50 days. In the control animals, tumor volume increased steadily, reaching approximately 3500 to 6000  $\text{mm}^3$  in size at the time of sacrifice, which was around day 32. By contrast, tumor volumes for



both experimental groups remained essentially constant up to 50 days, indicating that huKS-ala-IL2(N88R) was as effective as huKS-ala-IL2 in preventing tumor growth.

b) Treatment of a LLC/KSA subcutaneous tumor in C57BL/6 mice. In a second tumor model, a subcutaneous tumor was induced using Lewis Lung Carcinoma cells transduced with the gene encoding the KS antigen.  $1 \times 10^6$  viable LLC cells expressing EpCAM were suspended in 100  $\mu$ l of PBS and injected subcutaneously into the dorsa of 6-8 week old C57BL/6 mice. When tumor size reached 100-150  $\text{mm}^3$ , groups of eight mice were treated and evaluated as above, except that administered dose was increased to 20  $\mu$ g per injection. In the control animals, tumor volume increased rapidly, exceeding 6500  $\text{mm}^3$  in 20 days; the growth of the tumor for both experimental conditions was retarded to the same extent, reaching 4000  $\text{mm}^3$  over the same period, indicating again that there was no difference in efficacy between treatment with huKS-ala-IL2 and huKS-ala-IL2(N88R) at the same dose.

c) Treatment of a LLC/KSA subcutaneous tumor in B6.CB17-Prkdc<sup>scid</sup>/SzJ mice. The fusion proteins of the invention may also be effective on cells other than mature T cells. For example, in one experiment, the fusion proteins of the invention led to retardation of tumor growth even in mice that lack mature T-cells. These results suggest that the fusion proteins of the invention may be useful in the treatment of tumors in, for example, immunocompromised patients.

An LLC/KSA subcutaneous tumor model was evaluated in 11 week old B6.CB17-Prkdc<sup>scid</sup>/SzJ mice, which are compromised in their T-cell and B-cell mediated immune response. The same treatment protocol as described above was followed. Tumors in the control animals grew rapidly, to 3500  $\text{mm}^3$  in 15 days. Both huKS-ala-IL2 and huKS-ala-IL2 (N88R) were similarly effective in retarding tumor growth to less than half that size over the same period. Moreover, the differences in tumor growth rates between the C57BL/6 mice, which have an intact immune system, and the B6.CB17-Prkdc<sup>scid</sup>/SzJ mice, which lack T cells and B cells, were minimal.

Furthermore, the fact that KS-ala-IL2 led to the treatment of the tumor equally well in mice with an intact immune system and in mice lacking functional T cells, indicated that in this tumor model the immunologic response operated through a non-T cell mediated mechanism. Therefore, it is valuable to maintain in a therapeutic molecule the option to stimulate an immunologic response through a variety of effector cells. In the case of KS-ala-IL2(N88R), which was as effective as KS-ala-IL2 in either mouse background, effector cell activities that act independently of T cells were apparently preserved.

d) Treatment of LLC/KSA metastases to the lungs of C57BL/6 mice. LLC/KSA cells were also used in a lung metastasis model.  $1 \times 10^6$  viable cells were suspended in 200  $\mu$ l PBS and injected intravenously into 6-8 week old C57BL/6 mice. On day 4, groups of eight mice were subjected to one of the following treatment conditions: on five consecutive days, the mice were injected intravenously with 200  $\mu$ l PBS, or with 20  $\mu$ g of either KS-ala-IL2 or KS-ala-IL2(N88R) diluted into 200  $\mu$ l of PBS. The animals were sacrificed at about day 27, and lungs were dissected and fixed in Bouin's solution. The extent of metastasis in the lungs was evaluated by scoring the percentage of surface area covered by metastasis and by lung weight.

Lungs of the control group had over 96% of their surface area covered by metastases, and approximately a five-fold increase in lung weight (0.75 g) over a normal lung. By contrast, lungs of mice treated with huKS-ala-IL2 were mini-

mally covered with metastases (5.6%), and those of mice treated with huKS-ala-IL2(N88R) were virtually free of metastases (0%). Lungs of animals treated with huKS-ala-IL2 and huKS-ala-IL2(N88R) were of normal weight. Thus, huKS-ala-IL2(N88R) proved as efficacious as huKS-ala-IL2 in treating the lung metastases at a dose many fold lower than the threshold that would affect their survival.

#### Example 8

##### KS-IL2 Variants in Combination Therapy

The effect of administering a low toxicity KS-IL2 variant, such as huKS-ala-IL2(N88R), in conjunction with a second immuno-modulatory agent for the treatment of tumors was investigated, employing the subcutaneous tumor model LLC/KSA in mice as described in Example 7b.

a) huKS-ala-IL2 variants and cyclophosphamide. For the combination therapy, cyclophosphamide was administered intraperitoneally at a dose of 75 mg/kg on day 0, at which point the tumors averaged 90  $\text{mm}^3$ , and was followed by a daily administration of the fusion protein over five days (on day 1 through day 5). huKS-ala-IL2(N88R) was administered at either a 20  $\mu$ g or a 100  $\mu$ g dose. Control conditions included mock-treated animals and animals treated either with huKS-ala-IL2 alone at a 20  $\mu$ g dose, or with huKS-ala-IL2(N88R) alone at a 20  $\mu$ g or a 100  $\mu$ g dose. Tumors in mock-treated animals had progressed to about 5000  $\text{mm}^3$  by day 19, whereas tumors of mice treated with huKS-ala-IL2 were around 2200  $\text{mm}^3$ , and of mice treated with 20  $\mu$ g or 100  $\mu$ g of huKS-ala-IL2(N88R) were around 2600  $\text{mm}^3$  and 1700  $\text{mm}^3$  respectively. Co-administration of cyclophosphamide resulted in a tumor of 1700  $\text{mm}^3$  at the 20  $\mu$ g dose of huKS-ala-IL2(N88R) and of 1250  $\text{mm}^3$  at the higher dose, significantly smaller than the treatment with huKS-ala-IL2 alone.

b) huKS-ala-IL2 variants and indomethacin. For the combination therapy, indomethacin was administered orally at a dose of 35  $\mu$ g/mouse/day along with a daily administration of the fusion protein over five days (day 1 through day 5). Tumors initially averaged 90  $\text{mm}^3$ . huKS-ala-IL2(N88R) was administered at a 20  $\mu$ g dose. Control conditions included mock-treated animals and animals treated either with huKS-ala-IL2 alone at a 20  $\mu$ g dose, or with huKS-ala-IL2(N88R) alone at a 20  $\mu$ g dose. Tumors in mock-treated animals had progressed to about 5000  $\text{mm}^3$  by day 19, whereas tumors of mice treated with huKS-ala-IL2 were around 2200  $\text{mm}^3$ , and of mice treated with 20  $\mu$ g of huKS-ala-IL2(N88R) were around 2600  $\text{mm}^3$  and 1700  $\text{mm}^3$  respectively. Co-administration of indomethacin resulted in a decrease in tumor size to 850  $\text{mm}^3$  at the  $\mu$ g dose of huKS-ala-IL2(N88R), a significantly smaller tumor than obtained by treatment with huKS-ala-IL2 alone.

#### Example 9

##### KS-IL2 Variants with an Improved Therapeutic Index

KS-IL2 variants are constructed with mutations at particular positions in the IL-2 sequence. For example, substitutions are created at positions that are likely to interface with the  $\alpha$  subunit of IL-2 receptor. A suitable residue is, for example, F42 in the mature sequence of huIL-2. The aromatic ring structure of this amino acid is thought to stabilize the local conformation in IL-2 (Mott et al, JMB 1995, 247:979), and it is found that substitutions at this position with for instance Y, A or K in the immunocytokine lead to a molecule with pro-



gressively decreased IL-2 receptor affinity and bioactivity. These molecules are tested in animals and it is found that an increase in the therapeutic index in the treatment of tumors is achieved when compared with the unaltered form of the immunocytokine. Other substitutions that are effective are at positions R38 and K43.

Other substitutions in the IL-2 portion of the immunocytokine are in a region that is likely to interface with the  $\beta$  subunit, for example, at position E15 or L19 of the mature hu IL-2. When these residues are mutated to, for example, A or R in the immunocytokine it is found that the variant immunocytokines have a decreased affinity for the  $\beta$  subunit of the IL-2 receptor as compared to the unaltered form of the immunocytokine. It is generally found that the effects with substitutions to R are more severe than with substitutions to A, which may be related to the bulkiness of the side chain of R. These molecules are tested in animals and it is found that an increase in therapeutic index in the treatment of tumors is achieved when compared to the unaltered form of the immunocytokine. Other substitutions are introduced at positions D84 and V91 and are shown also to be effective in increasing the therapeutic index.

A substitution in the IL-2 portion of the immunocytokine that is likely to affect a region of the molecule that interfaces with the  $\gamma$  subunit of the IL-2 receptor is introduced at position N119 of the mature hu IL-2. A more subtle immunocytokine variant is created with a mutation to A and a more disruptive mutation is created with a mutation to R. The effect of these variants is tested in animals bearing tumors and it is found that these variant immunocytokines do have an improved therapeutic index as compared to the unaltered form of the immunocytokine.

It is also found that an increase in therapeutic index can be achieved by generating multiple mutations in the IL-2 immunocytokine, particularly for molecules where single mutations in the immunocytokine have shown only a marginal or negligible increase in therapeutic index. For example, an immunocytokine containing the combination F42A with L19A, or L19A with N119A, is found to be more effective than either immunocytokine variant alone. For an application involving multiple mutations, it is particularly useful to use mutations that decrease the size of an amino acid side chain. Another substitution introduced into the IL-2 portion of the immunocytokine is at T51 of the mature huIL-2. Whereas a mutation to A does not show an improvement in therapeutic index, the mutation to P creates an immunocytokine with improved therapeutic index when compared to the unaltered form of the immunocytokine in the treatment of tumors.

#### Example 10

##### Ig-IL2 Fusion Protein Variant huKS-ala-IL2(D20T) and Derivatives Thereof

Variants based on Ig-IL2(D20T), which contains the substitution of an aspartate to a threonine at position 20 of the mature huIL-2, were generated. These variants contain additional substitutions in the Ig domain, such as in the Fc portion or in the antibody targeting domains. To generate the DNA constructs encoding these molecules, procedures were followed essentially as described in Example 1, using a PCR approach with construct-specific primers to introduce the mutation and appropriate cloning strategies, familiar to those reasonably skilled in the art.

a) huKS-ala-IL2(D20T). To introduce the mutation D20T, a PCR mutagenesis approach was used with the primer set 5'-CAGCTGCAACTGGAGCATCTCCTGCT-GACCCTCCAGATGATTCTGAAT-3' (the bold nucleotides indicating the substituted codon) (SEQ ID NO: 28) and

primer T3 (5'-ATTAACCCTCACTAAAGGGA-3') (SEQ ID NO: 29), the DNA fragment was amplified from wild-type huIL-2 DNA on a pBS plasmid and inserted into a TA vector (Invitrogen) to generate TA-IL2(D20T). Mutagenesis was verified by sequencing. To substitute for the original IL-2 sequence in huKS-ala-IL2, a 385 bp PvuII/XhoI fragment from TA-IL2(D20T) was cloned into the parental immunocytokine plasmid in a triple ligation reaction. The fusion protein was expressed and purified essentially as described in Example 3. Amino acid sequences corresponding to hu-KS heavy and light chain variable regions are shown in SEQ ID NOs: 30 and 31 respectively.

Further variants of huKS-ala-IL2(D20T) were generated, incorporating the same PCR-derived fragment into different plasmid back-bones.

b) dI-KS-ala-IL2(D20T). A version of KS-ala-IL2 with an alteration removing a potential T-cell epitope has been previously described. The fusion protein was expressed and purified essentially as described in Example 3. The amino acid sequence corresponding to the heavy chain of the dI-KS antibody fused to the IL2(D20T) variant is depicted in SEQ ID NO: 32. SEQ ID NO: 33 and 34 correspond to the dI-KS heavy chain and light chain variable regions respectively.

c) De-glycosylated dI-KS-ala-IL2(D20T). Enzymatic deglycosylation using N-Glycanase was performed on the protein dI-KS-ala-IL2(D20T) essentially as described in Example 2.

d) dI-KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T). The Ig-moiety for this IL-2(D20T) fusion protein was derived from the constant region of an IgG  $\gamma$ 4 subclass (SEQ ID NO: 7), which in addition retained features of the IgG  $\gamma$ 1 hinge (SEQ ID NO: 10). Furthermore, mutations that remove potential T-cell epitopes were introduced. Additionally, this fusion protein contains the substitution from asparagine to glutamine, which eliminates the N-glycosylation site in Fc (see Example 4). The concomitant substitution of a phenylalanine to alanine removes the potential T-cell epitope. The fusion protein was expressed and purified essentially as described in Example 3.

e) dI-NHS76( $\gamma$ 2h)-ala-IL2(D20T). The Ig-moiety for this IL-2(D20T) fusion protein was derived from the constant region of an IgG  $\gamma$ 2 subclass, which in addition retained features of the IgG  $\gamma$ 1 hinge. In NHS76, the Ig variable regions are directed against epitopes contained in DNA-histone complexes and specifically recognize necrotic centers of tumors (Williams et al, PCT WO 00/01822). Also, a mutation that eliminates a potential T-cell epitope in the variable region of the light chain was introduced. This residue, leucine 104, lies at the CDR3 V-J junction, and was substituted by a valine. The fusion protein was expressed and purified essentially as described in Example 3.

f) dI-NHS76( $\gamma$ 2h)(FN>AQ)-ala-IL2(D20T). This protein, based on the protein of Example 10e, additionally contains the mutations that eliminate N-linked glycosylation in Fc and a potential T-cell epitope, as described in Example 10d. The fusion protein was expressed and purified essentially as described in Example 3. In one embodiment, fusion proteins of the invention include the heavy chain sequence of the NHS76( $\gamma$ 2h)(FN>AQ) molecule fused to the IL2(D20T) variant, as depicted in SEQ ID NO: 35, and the light chain variable and constant region sequence corresponding to SEQ ID NO: 36. However, the heavy chain region of SEQ ID NO: 35 can be used in combination with any IgG light chain variable or constant region.

g) dI-NHS76( $\gamma$ 4h)-ala-IL2(D20T). This protein is similar to the one described in Example 10e, but contains a heavy chain derived from the  $\gamma$ 4 rather than the  $\gamma$ 2 IgG subclass. The fusion protein was expressed and purified essentially as described in Example 3.

h) dI-NHS76( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T). This protein, based on the protein of Example 10g, additionally contains



the mutations that eliminate N-linked glycosylation in Fc and a potential T-cell epitope, as described in Example 10d. The fusion protein was expressed and purified essentially as described in Example 3. In one embodiment, fusion proteins of the invention include the heavy chain sequence of the dI-NHS76( $\gamma$ 4h)(FN>AQ) molecule fused to the IL-2(D20T) variant, depicted in SEQ ID NO: 37, and the light chain variable and constant region sequence corresponding to SEQ ID NO: 36. However, the heavy chain region of SEQ ID NO: 37 can be used in combination with any IgG light chain variable or constant region.

The Ig moiety of a fusion protein of the invention can include domains of heavy chain constant regions derived from any subclass of IgG, including combinations containing domains of IgG molecules derived from different species. Accordingly, the fusion proteins of the invention may include hinge regions derived from any subclass of IgG, for example, a hinge region derived from IgG gamma 1 (SEQ ID NO: 10), gamma 2 (SEQ ID NO: 11) or gamma 4 (SEQ ID NO: 12).

Activity of Ig-IL2(D20T) variants in bioassays: The Ig-IL2 (D20T) fusion proteins were tested in bioassays that measure the ability of cells dependent on IL-2 for growth to proliferate, which was expressed as an ED50 value (see Example 4). The assays were performed on murine CTLL-2 cells or human Kit-225 cells (which express IL-2R $\alpha\beta\gamma$ ), and human TF-1 $\beta$  cells or isolated murine NK cells (which express IL-2R $\beta\gamma$ ).

For example, in a representative experiment it was found that, compared to huKS-ala-IL2, the ED50 value for dI-KS-ala-IL2(D20T) in IL-2R $\alpha\beta\gamma$  bearing cells CTLL-2 was unchanged, whereas in IL-2R $\beta\gamma$  bearing cells TF-1 $\beta$  it was approximately 900-fold higher. The ED50 ratio, as defined in Example 4, therefore was around 150, revealing a shift of approximately 750-fold in selectivity towards IL-2R $\alpha\beta\gamma$  bearing CTLL-2 cells as compared to huKS-ala-IL2. Compared to the shift in selectivity of approximately 20,000-fold (relative to KS-ala-IL2) seen with huKS-ala-IL2(N88R) in this pair of cell lines, the selectivity was reduced about 10 to 20-fold for dI-KS-ala-IL2(D20T), which reflected the measurable proliferative response obtained from IL-2R $\beta\gamma$  expressing cells. This trend was also apparent when human Kit 225 cells were used. As was found with other Ig-fusion proteins containing the KS antibody, deglycosylation of the antibody portion had a small but consistent effect on reducing the activity of the fusion protein in IL-2R $\beta\gamma$  expressing cells.

IL-2 dependent cell proliferation was also measured in Ig-IL2(D20T) variants containing a different antibody moiety. It was found that, compared to dI-NHS76( $\gamma$ 2)-ala-IL2, the ED50 value for dI-NHS76( $\gamma$ 2)-ala-IL2(D20T) in IL-2R $\alpha\beta\gamma$  bearing cells Kit-225 was increased 3-fold, whereas in IL-2R $\beta\gamma$  bearing cells TF-1 $\beta$  it was increased approximately 230-fold. The resultant ED50 ratio of 350 was in the same range as was seen with dI-KS( $\gamma$ 4)(FN>AQ)-ala-IL2(D20T) and at least 10 fold less selective than huKS-ala-IL2(N88R). Representative results are shown in Table 4.

TABLE 4

Protein	ED50 Ratio TF-1 $\beta$ /CTLL-2	ED50 Ratio TF-1 $\beta$ /Kit-225
dI-KS-ala-IL2(D20T)	150	3000
dI-KS( $\gamma$ 4)(FN > AQ)-ala-IL2(D20T)		5600*
dI-NHS76( $\gamma$ 2)-ala-IL2(D20T)		350

\*= average of different lots

Pharmacokinetics of Ig-IL2(D20T) variants: To assess the interaction of Ig-IL2 variants with cell surface Fc receptors, binding of the Ig-IL2 fusion proteins to Fc $\gamma$ R receptors was

assayed in a cell-based ELISA, using U937 cells. Fusion proteins (huKS-ala-IL2, dI-huKS-ala-IL2, dI-KS-ala-IL2 (D20T), and dI-KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T)) were diluted 2-fold over a range from 100  $\mu$ g/ml to 780 ng/ml, incubated with the cells and binding was detected using FITC-conjugated antihuman IgG Fc Ab F(ab')<sub>2</sub> (Jackson Immunoresearch, West Grove, Pa.). The concentration of half-maximal binding of huKS-ala-IL2 and dI-KS-ala-IL2 for these cells was around 5  $\mu$ g/ml, and interestingly, was increased two-fold with dI-KS-ala-IL2(D20T) protein. While the introduction of the mutation that prevents glycosylation of the Ig moiety (dI-KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T)) reduced the binding of this protein to U973 cells 5- to 10-fold, binding was not completely abrogated.

The pharmacokinetic properties of the Ig-IL2(D20T) variants in mice were investigated, essentially as described in Example 5. Surprisingly, when compared to dI-KS-ala-IL2, the half-life of dI-KS-ala-IL2(D20T) was drastically reduced. Analysis of the PK profile indicated that the effect was particularly dramatic during the  $\alpha$ -phase: whereas 50% of dI-KS-ala-IL2 was still available after 1 hour, only approximately 5% of dI-KS-ala-IL2(D20T) was still present. The slopes of the  $\beta$ -phase of the PK profile for these proteins were similar. An essentially identical PK profile to the one seen with dI-KS-ala-IL2(D20T) was obtained with the fusion protein dI-NHS76( $\gamma$ 2h)-ala-IL2(D20T), which contains an IgG of subclass  $\gamma$ 2, that normally exhibits the least FcR binding affinity. Thus, the effect of the IL(D20T) protein moiety on the fusion protein was not limited to the antibody dI-KS.

Deglycosylation of an Ig fusion protein generally was observed to have the effect of enhancing the  $\alpha$ -phase of a PK profile. The effect of enzymatic deglycosylation of dI-KS-ala-IL2(D20T) on the PK profile was therefore investigated. In fact, the  $\alpha$ -phase of the PK profile was essentially restored to what had been observed with dI-KS-ala-IL2. The same effect was achieved when the glycosylation was abrogated by mutagenesis, as in the fusion protein dI-KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T). It is thus likely that the effect on the PK profile is due to reduced FcR binding.

Toxicity of Ig-IL2(D20T) variants: The toxicity of Ig-L2 (D20T) variant KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T) was compared to that of dI-KS-ala-IL2 in Balb/C mice, as described in Example 6.

Both fusion proteins had a similar serum half-life in mice. dI-( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T) was administered in five daily doses of either 100  $\mu$ g/mouse, 200  $\mu$ g/mouse or 400  $\mu$ g/mouse whereas dI-KS-ala-IL2 was administered in five daily doses of 40  $\mu$ g/mouse. It was found that the mice survived even a dose of 400  $\mu$ g/mouse of dI-KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T), whereas control mice, which received one tenth the dose of dI-KS-ala-IL2, had died by day 6. The body weights of the mice treated with dI-KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T) was slightly affected, dropping transiently to 97% of initial weight on day 7. A difference of more than 10-fold in the tolerated dose may indicate a substantial improvement in the therapeutic index.

Efficacy of Ig-IL2(D20T) variants for the treatment of tumors: The efficacy of Ig-IL2(D20T) variants was evaluated in Balb/C mice bearing a subcutaneous tumor derived from CT26/KSA cells, as described in Example 7a.

The fusion protein dI-KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T) was administered at doses of 15  $\mu$ g/mouse and 30  $\mu$ g/mouse. Tumors started at an average size of 126 mm<sup>3</sup> and reached sizes between 1800 mm<sup>3</sup> and 5000 mm<sup>3</sup> by day 28. Tumors in mice treated with 15  $\mu$ g/mouse of dI-KS-ala-IL2 had grown to an average size of 355 mm<sup>3</sup>, while tumors in mice treated with 15  $\mu$ g/mouse of dI-KS-ala-IL2(D20T) had reached an aver-



age size of 2250 mm<sup>3</sup>. This was most likely due to the poor PK of the molecule. Tumors in mice treated with dI-KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T) at the lower dose of 15  $\mu$ g/mouse had grown to some extent, to an average size of 1450 mm<sup>3</sup>; however, whereas at the 30  $\mu$ g/mouse dose tumors reached an average size of 950 mm<sup>3</sup>, significantly, in over half the mice the tumors had not grown appreciably. Thus, at increased doses dI-KS( $\gamma$ 4h)(FN>AQ)-ala-IL2(D20T) had a significant effect on inhibiting tumor growth. In fact, the dose used in this experiment was at least 12-fold lower than a maximal tolerated dose for this molecule and therefore it is likely to have an improved therapeutic index over the huKS-ala-IL2, which by comparison was administered at one third to one half of maximal tolerated dose.

#### Example 11

##### Relative Affinities of Wild-Type and Mutant IL-2 Fusion Proteins for Different IL-2 Receptors

Differential affinity of the various fusion proteins of the invention for an IL-2R $\beta\gamma$  receptor relative to an IL-2R $\alpha\beta\gamma$  receptor can be measured by an assay such as a radioimmunoassay. Equal numbers of IL-2R $\alpha\beta\gamma$  receptor expressing cells or IL-2R $\beta\gamma$  receptor expressing cells are plated on plastic plates. A dilution series is performed with an equal amount of either wild-type or mutant IL-2 fusion protein added to equal numbers of IL-2R $\alpha\beta\gamma$  receptor expressing cells or IL-2R $\beta\gamma$  receptor expressing cells in order to obtain a standard curve. Unbound fusion proteins are washed away and the amount of fusion protein bound to each cell type is detected by a radiolabelled ligand. In the case of an Fc-IL-2 fusion protein, the ligand can be a molecule such as a staphylococcal protein A which binds to the Fc portion of an IgG. The ligand can also be another antibody that recognizes a portion of a particular subclass of the IgG molecule, for example, antibodies to IgG gamma 1, IgG gamma 2 or IgG gamma 4 constant regions. Unbound ligand is washed away and radioactivity of the plate containing either IL-2R $\alpha\beta\gamma$  expressing

cells bound with wild-type IL-2 fusion protein; IL-2 $\alpha\beta\gamma$  expressing cells bound with mutant IL-2 fusion protein; IL-2R $\beta\gamma$  expressing cells bound with wild-type IL-2 fusion protein or IL-2R $\beta\gamma$  expressing cells bound with mutant fusion protein is measured on a gamma counter. The data obtained from the binding assay is normalized to account for the number of cells and receptors expressed on the cells.

In yet another assay, the fusion proteins themselves can be labeled, either radioactively, or non-radioactively using a variety of techniques well known in the art. Similar to the assay described above for a labeled ligand, either wild-type or mutant labeled fusion protein is added to equal number of plated cells and the amount of labeled fusion protein is measured.

The binding affinity of a fusion protein for a particular receptor is measured by the ratio of the concentration of the bound ligand or bound fusion protein, as described above, to the product of the concentration of unbound ligand or unbound fusion protein and the total concentration of the fusion protein added to each reaction. When compared to a wild-type IL-2 fusion protein, certain mutations in the IL-2 moiety alter the fusion protein's relative affinity for an IL-2R $\beta\gamma$  receptor and an IL-2R $\alpha\beta\gamma$  receptor.

#### EQUIVALENTS

The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are therefore to be considered in all respects illustrative rather than limiting on the invention described herein. Scope of the invention is thus indicated by the appended claims rather than by the foregoing description and all changes which come within the meaning and range of equivalency of the claims are intended to be embraced therein.

All patents, patent applications and scientific publications referenced to herein are incorporated by reference in their entirety.

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#### SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 37

<210> SEQ ID NO 1  
 <211> LENGTH: 7  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: IgG gamma 1 sequence

<400> SEQUENCE: 1

Gln Tyr Asn Ser Thr Tyr Arg  
 1 5

<210> SEQ ID NO 2  
 <211> LENGTH: 5  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Ig Gamma 2 or 4 sequence

<400> SEQUENCE: 2

Gln Phe Asn Ser Thr  
 1 5



-continued

<210> SEQ ID NO 3  
 <211> LENGTH: 133  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His  
 1 5 10 15  
 Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys  
 20 25 30  
 Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys  
 35 40 45  
 Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys  
 50 55 60  
 Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu  
 65 70 75 80  
 Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu  
 85 90 95  
 Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala  
 100 105 110  
 Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile  
 115 120 125  
 Ile Ser Thr Leu Thr  
 130

<210> SEQ ID NO 4  
 <211> LENGTH: 12  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Xma I site created in the human gamma-1 heavy  
 chain gene

<400> SEQUENCE: 4

tccccgggta aa

12

<210> SEQ ID NO 5  
 <211> LENGTH: 7  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: wild-type huKS-ala-1L2 junction

<400> SEQUENCE: 5

Ser Pro Gly Lys Ala Pro Thr  
 1 5

<210> SEQ ID NO 6  
 <211> LENGTH: 7  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: mutant huKS-ala-1L2 junction

<400> SEQUENCE: 6

Ser Gly Pro Ala Ala Pro Thr  
 1 5

<210> SEQ ID NO 7  
 <211> LENGTH: 327  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens



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<220> FEATURE:
<221> NAME/KEY: misc
<222> LOCATION: (1)..(327)
<223> OTHER INFORMATION: Human gamma 4 constant region

<400> SEQUENCE: 7

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1          5          10          15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20          25          30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35          40          45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50          55          60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65          70          75          80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85          90          95
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100         105         110
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115         120         125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130         135         140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145         150         155         160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165         170         175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180         185         190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195         200         205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210         215         220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225         230         235         240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245         250         255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260         265         270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275         280         285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290         295         300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305         310         315         320
Leu Ser Leu Ser Leu Gly Lys
325

<210> SEQ ID NO 8
<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc
<222> LOCATION: (1)..(330)
<223> OTHER INFORMATION: IgG1 constant region

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&lt;400&gt; SEQUENCE: 8

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 1 5 10 15  
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95  
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 100 105 110  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 115 120 125  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 130 135 140  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
 145 150 155 160  
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 165 170 175  
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
 180 185 190  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 195 200 205  
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
 210 215 220  
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
 225 230 235 240  
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 245 250 255  
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 260 265 270  
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 275 280 285  
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
 290 295 300  
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
 305 310 315 320  
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 325 330

&lt;210&gt; SEQ ID NO 9

&lt;211&gt; LENGTH: 326

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: misc

&lt;222&gt; LOCATION: (1)..(326)

&lt;223&gt; OTHER INFORMATION: Human gamma 2 constant region

&lt;400&gt; SEQUENCE: 9

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg







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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Human IgG gamma 2 hinge region

<400> SEQUENCE: 11

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro  
 1 5 10

<210> SEQ ID NO 12  
 <211> LENGTH: 12  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Human IgG gamma 4 hinge region

<400> SEQUENCE: 12

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro  
 1 5 10

<210> SEQ ID NO 13  
 <211> LENGTH: 9  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: C-terminal of Ig G gamma 1 and gamma 2 constant regions

<400> SEQUENCE: 13

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 1 5

<210> SEQ ID NO 14  
 <211> LENGTH: 9  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: C-terminal of IgG gamma 4 constant region

<400> SEQUENCE: 14

Lys Ser Leu Ser Leu Ser Leu Gly Lys  
 1 5

<210> SEQ ID NO 15  
 <211> LENGTH: 9  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: mutated C-terminal of IgG gamma constant regions

<400> SEQUENCE: 15

Lys Ser Ala Thr Ala Thr Pro Gly Ala  
 1 5

<210> SEQ ID NO 16  
 <211> LENGTH: 32  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: sense primer for generating huKS-ala-IL2 (N88R) fusion protein

<400> SEQUENCE: 16

ccccgggtgc cgccccaact tcaagttcta ca

32

<210> SEQ ID NO 17  
 <211> LENGTH: 53



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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: antisense primer for generating the  
 huKS-ala-IL2(N88R) fusion protein

<400> SEQUENCE: 17

agccctttag ttccagaact attacgttga tctgctgat taagtccta ggt 53

<210> SEQ ID NO 18  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: second sense primer

<400> SEQUENCE: 18

agttctggaa ctaaaggct cggaaacaac attcatgtgt 40

<210> SEQ ID NO 19  
 <211> LENGTH: 4  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: mutant sequence in huKS M1 IL-2 variant

<400> SEQUENCE: 19

Thr Thr Ser Arg  
 1

<210> SEQ ID NO 20  
 <211> LENGTH: 12  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: antibody-IL-2 junction sequence

<400> SEQUENCE: 20

Lys Ser Leu Ser Leu Ser Pro Gly Ala Ala Pro Thr  
 1 5 10

<210> SEQ ID NO 21  
 <211> LENGTH: 12  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: mutant antibody-IL-2 junction sequence

<400> SEQUENCE: 21

Lys Ser Ala Thr Ala Thr Pro Gly Ala Ala Pro Thr  
 1 5 10

<210> SEQ ID NO 22  
 <211> LENGTH: 6  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: sequence in huKS M1-IL2 variant

<400> SEQUENCE: 22

Asp Leu Ile Ser Asn Ile  
 1 5

<210> SEQ ID NO 23  
 <211> LENGTH: 6  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence



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<220> FEATURE:  
 <223> OTHER INFORMATION: mutant sequence in huKS M1-IL2 variant

<400> SEQUENCE: 23

Asp Thr Thr Ser Arg Ile  
 1                   5

<210> SEQ ID NO 24  
 <211> LENGTH: 43  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: sense primer for generating the N88R mutation

<400> SEQUENCE: 24

acttaagacc tagggacacc accagcagga tcaacgtaat agt 43

<210> SEQ ID NO 25  
 <211> LENGTH: 18  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: antisense primer for N88R mutation

<400> SEQUENCE: 25

atcatgtctg gatccctc 18

<210> SEQ ID NO 26  
 <211> LENGTH: 7  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: N to Q mutation in the CH2 domain of the Fc  
 gamma 1 constant region

<400> SEQUENCE: 26

Gln Tyr Gln Ser Thr Tyr Arg  
 1                   5

<210> SEQ ID NO 27  
 <211> LENGTH: 5  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: FN to AQ mutation in Fc portion of gamma 2 or 4  
 constant regions

<400> SEQUENCE: 27

Gln Ala Gln Ser Thr  
 1                   5

<210> SEQ ID NO 28  
 <211> LENGTH: 48  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: sense primer for D20T mutation

<400> SEQUENCE: 28

cagctgcaac tggagcatct cctgctgacc ctccagatga ttctgaat 48

<210> SEQ ID NO 29  
 <211> LENGTH: 20  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: antisense primer for D20T mutation



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&lt;400&gt; SEQUENCE: 29

attaaccctc actaaagga

20

&lt;210&gt; SEQ ID NO 30

&lt;211&gt; LENGTH: 116

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: hu-KS heavy chain variable region

&lt;400&gt; SEQUENCE: 30

Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
20 25 30Gly Met Asn Trp Val Lys Gln Thr Pro Gly Lys Gly Leu Lys Trp Met  
35 40 45Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe  
50 55 60Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Thr Ser Thr Ala Phe  
65 70 75 80Leu Gln Ile Asn Asn Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys  
85 90 95Val Arg Phe Ile Ser Lys Gly Asp Tyr Trp Gly Gln Gly Thr Ser Val  
100 105 110Thr Val Ser Ser  
115

&lt;210&gt; SEQ ID NO 31

&lt;211&gt; LENGTH: 106

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: hu-KS light chain variable region

&lt;400&gt; SEQUENCE: 31

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15Glu Arg Val Thr Leu Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met  
20 25 30Leu Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Phe  
35 40 45Asp Thr Ser Asn Leu Ala Ser Gly Phe Pro Ala Arg Phe Ser Gly Ser  
50 55 60Gly Ser Gly Thr Ser Tyr Ser Leu Ile Ile Ser Ser Met Glu Ala Glu  
65 70 75 80Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser Gly Tyr Pro Tyr Thr  
85 90 95Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

&lt;210&gt; SEQ ID NO 32

&lt;211&gt; LENGTH: 579

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

<223> OTHER INFORMATION: dI-KS-ala IL2 (D20T) heavy chain fused to IL-2  
variant



-continued

&lt;400&gt; SEQUENCE: 32

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
 20 25 30  
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Lys Trp Met  
 35 40 45  
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Thr Ala Glu Thr Ser Thr Ser Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Leu Asn Asn Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys  
 85 90 95  
 Val Arg Phe Ile Ser Lys Gly Asp Tyr Trp Gly Gln Gly Thr Thr Val  
 100 105 110  
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
 115 120 125  
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
 130 135 140  
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
 145 150 155 160  
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
 165 170 175  
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu  
 180 185 190  
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
 195 200 205  
 Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
 210 215 220  
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
 225 230 235 240  
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
 245 250 255  
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
 260 265 270  
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 275 280 285  
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val  
 290 295 300  
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
 305 310 315 320  
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 325 330 335  
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
 340 345 350  
 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
 355 360 365  
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 370 375 380  
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp  
 385 390 395 400  
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
 405 410 415



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Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
 420 425 430

Asn His Tyr Thr Gln Lys Ser Ala Thr Ala Thr Pro Gly Ala Ala Pro  
 435 440 445

Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu  
 450 455 460

Leu Thr Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro  
 465 470 475 480

Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala  
 485 490 495

Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu  
 500 505 510

Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro  
 515 520 525

Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly  
 530 535 540

Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile  
 545 550 555 560

Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser  
 565 570 575

Thr Leu Thr

<210> SEQ ID NO 33  
 <211> LENGTH: 116  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: dI-KS heavy chain variable region

&lt;400&gt; SEQUENCE: 33

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Ser  
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Lys Trp Met  
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe  
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Ala Glu Thr Ser Thr Ser Thr Leu Tyr  
 65 70 75 80

Leu Gln Leu Asn Asn Leu Arg Ser Glu Asp Thr Ala Thr Tyr Phe Cys  
 85 90 95

Val Arg Phe Ile Ser Lys Gly Asp Tyr Trp Gly Gln Gly Thr Thr Val  
 100 105 110

Thr Val Ser Ser  
115

<210> SEQ ID NO 34  
 <211> LENGTH: 106  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: dI-KS light chain variable region

&lt;400&gt; SEQUENCE: 34

Gln Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly  
 1 5 10 15



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Gln Arg Ala Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Ile  
 20 25 30  
 Leu Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Pro Trp Ile Phe  
 35 40 45  
 Asp Thr Ser Asn Leu Ala Ser Gly Phe Pro Ser Arg Phe Ser Gly Ser  
 50 55 60  
 Gly Ser Gly Thr Ser Tyr Thr Leu Thr Ile Asn Ser Leu Glu Ala Glu  
 65 70 75 80  
 Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser Gly Tyr Pro Tyr Thr  
 85 90 95  
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105

&lt;210&gt; SEQ ID NO 35

&lt;211&gt; LENGTH: 580

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: dI-NHS76 (gamma2h) (FN&gt;AQ) -ala-IL2(D20T) heavy chain fused to IL2 variant

&lt;400&gt; SEQUENCE: 35

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly  
 20 25 30  
 Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
 35 40 45  
 Ile Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu  
 50 55 60  
 Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser  
 65 70 75 80  
 Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Gly Lys Trp Ser Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110  
 Val Thr Val Ser Ser Gly Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
 115 120 125  
 Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly  
 130 135 140  
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
 145 150 155 160  
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
 165 170 175  
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser  
 180 185 190  
 Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser  
 195 200 205  
 Asn Thr Lys Val Asp Lys Thr Val Glu Pro Lys Ser Cys Asp Lys Thr  
 210 215 220  
 His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val  
 225 230 235 240  
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
 245 250 255  
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu



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260					265					270					
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Ala	Gln	Ser	Thr	Phe	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345					350		
Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370						375				380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser
385						390					395				400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
				405					410					415	
Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Ala	Thr	Ala	Thr	Pro	Gly	Ala	Ala
		435					440					445			
Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu
	450					455					460				
Leu	Leu	Thr	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn
465						470					475				480
Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Met	Pro	Lys	Lys
				485					490					495	
Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro
			500					505					510		
Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu	Arg
		515					520					525			
Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu	Lys
	530					535					540				
Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala	Thr
545						550					555				560
Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile	Ile
				565					570					575	
Ser	Thr	Leu	Thr												
		580													

&lt;210&gt; SEQ ID NO 36

&lt;211&gt; LENGTH: 229

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

<223> OTHER INFORMATION: dI-NHS76 (gamma4th) (FN>AQ)-ala-IL2 (D20T)  
variable light chain region

&lt;400&gt; SEQUENCE: 36

Ser	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln
1				5					10					15	

Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala
			20					25					30		



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Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr  
 35 40 45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser  
 50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu  
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His  
 85 90 95

Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gly His Gln  
 100 105 110

Asp Ser Asp Pro Leu Pro Leu Ile His Pro Ala Gly Gln Pro Lys Ala  
 115 120 125

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala  
 130 135 140

Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala  
 145 150 155 160

Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val  
 165 170 175

Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser  
 180 185 190

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr  
 195 200 205

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala  
 210 215 220

Pro Thr Glu Cys Ser  
 225

&lt;210&gt; SEQ ID NO 37

&lt;211&gt; LENGTH: 580

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: dI-NHS76(gamma4h)(FN&gt;AQ)-ala-IL2(D20T) heavy chain fused to IL-2 variant

&lt;400&gt; SEQUENCE: 37

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly  
 20 25 30

Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
 35 40 45

Ile Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu  
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser  
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Gly Lys Trp Ser Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys  
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160



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Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 180 185 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn  
 195 200 205

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His  
 210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val  
 225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
 245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu  
 260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
 275 280 285

Thr Lys Pro Arg Glu Glu Gln Ala Gln Ser Thr Tyr Arg Val Val Ser  
 290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys  
 305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile  
 325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
 340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
 355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn  
 370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
 385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
 405 410 415

Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu  
 420 425 430

His Asn His Tyr Thr Gln Lys Ser Ala Thr Ala Thr Pro Gly Ala Ala  
 435 440 445

Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu  
 450 455 460

Leu Leu Thr Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn  
 465 470 475 480

Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys  
 485 490 495

Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro  
 500 505 510

Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg  
 515 520 525

Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys  
 530 535 540



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Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala	Thr
545					550					555					560
Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile	Ile
				565					570					575	
Ser	Thr	Leu	Thr												
			580												

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The invention claimed is:

**1.** A DNA encoding a fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2 moiety,

wherein the mutant IL-2 moiety comprises an amino acid substitution changing an aspartic acid to a threonine at a position corresponding to position 20 of a mature human IL-2 protein,

wherein the mature human IL-2 protein consists of the amino acid sequence set forth in SEQ ID NO:3,

wherein said fusion protein exhibits greater selectivity than a reference protein towards cells expressing a high affinity receptor,

wherein said reference protein comprises the non-IL-2 moiety fused to a non-mutant IL-2 moiety, and

wherein said selectivity is measured as a ratio of activation of cells expressing IL-2R $\alpha\beta\gamma$  receptor relative to activation of cells expressing IL-2R $\beta\gamma$  receptor.

**2.** The DNA of claim **1**, wherein the selectivity is between about 0.1% to about 100% of selectivity of a reference fusion protein comprising the non-IL-2 moiety fused to a mutant human IL-2 moiety with an N to R amino acid substitution at position 88 of the mature human IL-2 protein consisting of the amino acid sequence set forth in SEQ ID NO:3.

**3.** The DNA of claim **1**, wherein the selectivity is between about 0.1% to about 30% of selectivity of a reference fusion protein comprising the non-IL-2 moiety fused to a mutant human IL-2 moiety with an N to R amino acid substitution at position 88 of the mature human IL-2 protein consisting of the amino acid sequence set forth in SEQ ID NO:3.

**4.** The DNA of claim **1**, wherein the selectivity is between about 1% to about 20% of selectivity of a reference fusion protein comprising a non-IL2 moiety fused to a mutant human IL-2 moiety with an N to R amino acid substitution at position 88 of the mature human IL-2 protein consisting of the amino acid sequence set forth in SEQ ID NO:3.

**5.** The DNA of claim **1**, wherein the selectivity is between about 2% to about 10% of selectivity of a reference fusion protein comprising a non-IL-2 moiety fused to a mutant human IL-2 moiety with an N to R amino acid substitution at position 88 of the mature human IL-2 protein consisting of the amino acid sequence set forth in SEQ ID NO:3.

**6.** The DNA of claim **1**, wherein the cells expressing IL-2R $\alpha\beta\gamma$  receptor are selected from the group consisting of CTLL-2, Kit 225 and mature T-cells.

**7.** The DNA of claim **1**, wherein the cells expressing IL-2R $\beta\gamma$  receptor are selected from the group consisting of TF-1 $\beta$  cells and NK cells.

**8.** The DNA of claim **1**, wherein the fusion protein has a longer serum half-life than mature human IL-2 protein.

**9.** The DNA of claim **1**, wherein the non-IL-2 moiety is albumin.

**10.** The DNA of claim **1**, wherein the non-IL-2 moiety comprises an antibody.

**11.** The DNA of claim **10**, wherein the DNA encodes an amino acid sequence selected from the group consisting of SEQ ID NO: 32, SEQ ID NO: 36, and SEQ ID NO: 37.

**12.** The DNA of claim **10**, wherein the non-IL-2 moiety is selected from the group consisting of KS-1/4, dI-KS, dI-KS ( $\gamma$ 4h)(FN>AQ), huKS, huKS(N to Q), NHS76( $\gamma$ 2h), NHS ( $\gamma$ 4h) NHS76( $\gamma$ 2h)(FN>AQ), NHS76( $\gamma$ 4h)(FN>AQ), and 14.18.

**13.** The DNA of claim **12**, wherein said mutant IL-2 moiety further comprises an amino acid substitution changing an asparagine to an arginine corresponding to position 88 of the mature human IL-2 protein consisting of the amino acid sequence set forth in SEQ ID NO:3.

**14.** The DNA of claim **13**, wherein said fusion protein further comprises an amino acid substitution changing a leucine to a threonine at position 85 and an amino acid substitution changing an isoleucine to a threonine corresponding to position 86 of the mature human IL-2 protein consisting of the amino acid sequence set forth in SEQ ID NO:3.

**15.** The DNA of claim **1**, wherein said mutant IL-2 moiety further comprises a mutation corresponding to an amino acid position of mature human IL-2 protein consisting of the amino acid sequence set forth in SEQ ID NO:3, the amino acid position being selected from the group consisting of lysine 8, glutamine 13, glutamic acid 15, histidine 16, leucine 19, glutamine 22, methionine 23, asparagine 26, histidine 79, leucine 80, arginine 81, aspartic acid 84, asparagine 88, isoleucine 92 and glutamic acid 95.

**16.** The DNA of claim **1**, wherein said mutant IL-2 moiety further comprises mature human IL-2 protein with a mutation corresponding to an amino acid position of mature human IL-2 protein consisting of the amino acid sequence set forth in SEQ ID NO:3, the amino acid position selected from the group consisting of leucine 25, asparagine 31, leucine 40, methionine 46, lysine 48, lysine 49, threonine 51, aspartic acid 109, glutamic acid 110, alanine 112, threonine 113, valine 115, glutamic acid 116, asparagine 119, arginine 120, isoleucine 122, threonine 123, glutamine 126, serine 127, serine 130 and threonine 131.

**17.** The DNA of claim **16**, wherein the amino acid mutation is an amino acid substitution changing a glutamine to an aspartic acid corresponding to position 126 of the mature human IL-2 protein consisting of the amino acid sequence set forth in SEQ ID NO:3.

**18.** The DNA of claim **1**, wherein the non-IL-2 moiety comprises an antibody constant domain.

**19.** The DNA of claim **18**, wherein the antibody constant domain comprises an IgG gamma-1 domain, an IgG gamma-2 domain or an IgG gamma-4 domain.

**20.** The DNA of claim **18**, wherein said antibody constant domain comprises a mutation.

**21.** The DNA of claim **20**, wherein the antibody constant domain comprises the amino acid sequence set forth in SEQ



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ID NO:1, but wherein the mutation changes the asparagine of SEQ ID NO:1 to a different amino acid.

**22.** The DNA of claim **21**, wherein said asparagine is changed to a glutamine.

**23.** The DNA of claim **20**, wherein the antibody constant domain comprises the amino acid sequence set forth in SEQ ID NO:2, but wherein the mutation changes the phenylalanine of SEQ ID NO:2 to an alanine and changes the asparagine of SEQ ID NO:2 to glutamine.

**24.** An isolated cell comprising the DNA of claim **1**.

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**25.** A method for producing a fusion protein, the method comprising the steps of:

maintaining the cell of claim **24** under conditions permitting expression of the fusion protein; and  
purifying the fusion protein.

**26.** The isolated cell of claim **24**, wherein the DNA encodes an amino acid sequence selected from the group consisting of SEQ ID NO: 32, SEQ ID NO: 36, and SEQ ID NO: 37.

\* \* \* \* \*